

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 02:35:09 ; Search time 19705 Seconds
(without alignments)
11620.464 Million cell updates/sec

Title: US-09-921-143-36

Perfect score: 5283

Sequence: 1 aagcttgacattatgagact.....tgagtgttcggcagcggtg 5283

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

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41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2410	45.6	6074	12	CVE18316
2	2240	42.4	8349	6	AR260588
3	2233.4	42.3	2661	12	SYNCKMRCG
4	2218.4	42.0	2999	12	SYNCCDBA
5	2218.4	42.0	2999	12	SYNCCDBB
6	2177.4	41.2	2604	12	AY189826
7	2177.4	41.2	11373	12	AY189827
8	2177.4	41.2	11403	12	AY189829
9	2088.4	39.5	3036	12	AY222815
10	2088.4	39.5	3210	12	AY219859
11	2088.4	39.5	5695	12	AY222822
12	2088.4	39.5	5869	12	AY219861
13	2088	39.5	5695	12	AF445080
14	2078	39.3	3035	12	AY222814
15	2078	39.3	3053	12	AY222811
16	1892	35.8	7020	12	AS293724
17	1793.4	33.9	4800	6	AR282049
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25	1669.6	31.6	5025	12	EC07659
26	1652.4	31.3	5594	6	AR214682
27	1644.6	31.1	2959	12	AF402779
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29	1618.2	30.6	6561	6	AR214683
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32	1602.2	30.3	3600	6	BD063789
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34	1600	30.3	5966	6	BD136050
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45	1570	29.7	5619	6	AX008865

ALIGNMENTS

RESULT 1	CVE18316	Cloning vector pKGM1.	6074 bp	DNA	linear	SYN 02-SEP-1999
LOCUS	CVE18316	Cloning vector pKGM1.	6074 bp	DNA	linear	SYN 02-SEP-1999
DEFINITION	Y18316					
ACCESSION	Y18316.1	GI:5830187				
VERSION	bleomycin resistance;	cloning vector; kanamycin resistance;				
KEYWORDS	multiple cloning site; neomycin resistance.					
SOURCE	Cloning vector pKGM1					
ORGANISM	Cloning vector pKGM1					
REFERENCE	artificial sequences; vectors.					
AUTHORS	1					
TITLE	Bannasch, D. and Schwab, M.					
JOURNAL	A versatile bait vector for rapid Gal4 dependent two-hybrid screens					
	Unpublished					

Pred. No. is the number of results predicted by chance to have a

2 (bases 1 to 6074)
Bannasch, D.
Direct Submission
Submitted (30-OCT-1998) D. Bannasch, Institution Division of,
Cytogenetics/H0400 Deutsches, Krebsforschungszentrum (DKFZ), Im
Neuenheimer Feld 280, D-69120 Heidelberg, FRG
Revised by author 10-JUN-1999
Related sequences U07646, U00004, L19385.
FEATURES
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Best Local Similarity 94.5%; Pred. No. 0;
Matches 2568; Conservative 0; Mismatches 5; Indels 145; Gaps 1;
QY 2711 CGTAATCATGTGCTAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAAATCCACACA 2770
DB 1954 CGTAATCATGTGCTAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAAATCCACACA 2013
QY 2771 ACATACGACCGGAAGCATAAAGTGTAAAGCCTGGGTGCCCTAATGAGTGAGCTAACTCA 2830
DB 2014 ACATACGACCGGAAGCATAAAGTGTAAAGCCTGGGTGCCCTAATGAGTGAGTGAGCTCA 2073
QY 2831 CATTAATTGGCTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTCGCAGCTGC 2890
DB 2074 CATTAATTGGCTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTCGCAGCTGC 2133
QY 2891 ATTAANGAATCGGCCAAACCGCGCGGAGAGAGCGGTTTCGGTATTGGGCGCTCTTCGCGTT 2950
DB 2134 ATTAATGAATCGGCCAAACCGCGCGGAGAGAGCGGTTTCGGTATTGGGCGCTCTTCGCGTT 2193

QY	3066	GTGAGCAAAAGCCAGCAAAAAGCCAGGAAACGGTAAAAAGCCCGCTTGTCTGGCGTTTTT	3125	Db	7207	AACCTCGTCAAGAAAGCGATAGAAAGCGGATCGCTCGGAATCGGAGCGCGATACCGTAA	7266
Db	6271	GTAGCAAAAGCCAGCAAAAAGCCAGGAAACCGTAAAAAGCCCGCTTGTCTGGCGTTTTT	6330	QY	4206	AGCAGAGAAAGCGGTAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGCGGTAGCC	4265
QY	3126	CCATAGGCTCCGCCCCCTGAGAGCATCACAAAATCGAGCTCAAGTCAGAGTGGCG	3185	Db	7267	AGCAGAGAAAGCGGTAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGCGGTAGCC	7326
Db	6331	CCATAGGCTCCGCCCCCTGAGAGCATCACAAAATCGAGCTCAAGTCAGAGTGGCG	6390	QY	4266	AACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGCCACACGTCTGATGAATCCAGAA	4325
QY	3186	AAACCCGACAGGACTATAAGATACAGCGGTTTCCCCCTGGAAGCTCCCTCGTGGCTC	3245	Db	7327	AACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGCCACACGTCTGATGAATCCAGAA	7386
Db	6391	AAACCCGACAGGACTATAAGATACAGCGGTTTCCCCCTGGAAGCTCCCTCGTGGCTC	6450	QY	4326	AAGCGGCCATTTTCCACCATGATATTCCGGAAGAGGCAATCCCATGGGTGACGAGAGA	4385
QY	3246	TCCTGTTCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGGT	3305	Db	7387	AAGCGGCCATTTTCCACCATGATATTCCGGAAGAGGCAATCCCATGGGTGACGAGAGA	7446
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Db	6631	TCGCTTTGAGTCCAAACCCCGTAAAGACAGCACTTATCGCACTGGCAGAGCCACTGGTAA	6690	QY	4566	AGCCCGCATTTGCATCAGCCATGATGTTCTCGGAGGCAAGGTAGATGAC	4625
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DEFINITION Cloning vector pKIL18 ccdB gene, complete cds and kanamycin-resistance (KmR) gene fragment.

ACCESSION L38498

VERSION L38498.1

KEYWORDS GI:986977

SOURCE ccdB gene; cloning vector; kanamycin resistance.

ORGANISM Cloning vector pKIL18

REFERENCE Cloning vector pKIL18

1 (bases 1 to 2999)

1. Bernard, P.

2. New ccdB positive-selection cloning vectors with kanamycin or chloramphenicol selectable markers

3. Gene 162 (1), 159-160 (1995)

4. 96009896

5. 7557407

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 42.0%; Score 2218.4; DB 12; Length 2999;

Best Local Similarity 93.4%; Pred. No. 0;

Matches 2388; Conservative 0; Mismatches 26; Indels 144; Gaps 1;

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2999 AGCTGTTTCTGTGAAATTTGTTATCCGCTCAATTCACACATACGAGCGGAA 2940

2786 GCATAAGTGAAGCCTGGGTGCTTAATGAGTGAGCTAACTCAATTAATTCGCTTC 2845

2939 GCATAAGTGAAGCCTGGGTGCTTAATGAGTGAGCTAACTCAATTAATTCGCTTC 2880

2846 GCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTCGCAAGTCAATTAATTCGCTTC 2905

2879 GCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTCGCAAGTCAATTAATTCGCTTC 2820

2906 AAGCGCGGGAGAGCGGTTTGGTAATGGCGCTCTTCGGCTTCCTCGCTCACTGACT 2965

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2759 CGCTGCGCTCGGTGCTTCGGCTGGCGAGCGGTATCAGTCACTCAAAAGCGGTAAATAC 2700

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2639 AGGCCAGGAACCGGTAAAGAGCGGTTGCTGGGCTTTTCCATAGGCTCGGCCCTCGT 2580

3146 ACGAGCATCAAAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACAGACTATATAA 3205

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4691 GAGCAGCTGCGCAAGAACCGCGCTGTCGCGACGACGATGCGCGCTGCTTCGCTC 4750

607 GAGCAGCTGCGCAAGAACCGCGCTGTCGCGACGACGATGCGCGCTGCTTCGCTC 548

4751 CTCGAGTTTATTCAGGCGACCGGACAGTTCGCTTCGACAAAAGAACCGCGCGCCCTG 4810

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4931 CATGCGAAACGATCTCTCATCTGCTCTTGATCAGATCTTTGATCCCTCGCGCATCAGAT 4990

367 CATGCGAAACGATCTCTCATCTGCTCTTGATCAGATCTTTGATCCCTCGCGCATCAGAT 308

4991 CTTTGGCGGAAAGAACGATTCAGTTTACTTTGAGGGCTTCCCAACCTTACAGAGG 5050

307 CTTTGGCGGAAAGAACGATTCAGTTTACTTTGAGGGCTTCCCAACCTTACAGAGG 248

5051 GCGCCGAGCTGGCAATTCGGTTCGCTGCTCCATAAAACCGCCAGTCTAGCTATCG 5110

247 GCGCCGAGCTGGCAATTCGGTTCGCTGCTCCATAAAACCGCCAGTCTAGCTATCG 188

5111 CCATGTAAGCCCACTGCAAGTACTGCTTTCTCTTTGCGCTTCGCTTTCCCTTTGCTCA 5170

187 CCATGTAAGCCCACTGCAAGTACTGCTTTCTCTTTGCGCTTCGCTTTCCCTTTGCTCA 128

5171 GATAGCCAGTATGATGATTCATTCGCGGAGTTCAGTTCGCGAGTTCGCTTTCTA 5230

127 GATAGCCAGTATGATGATTCATTCGCGGAGTTCAGTTCGCGAGTTCGCTTTCTA 68

5231 CGTCTCGCTTCCTTTAGCAGCCTTCGCGCCTGAGTTCGCTTTGGGAGCGCTG 5283

67 CGTCTCGCTTCCTTTAGCAGCCTTCGCGCCTGAGTTCGCTTTGGGAGCGCTG 15

RESULT 4

SYNCCDBA/c

LOCUS

SYNCCDBA

2999 bp

DNA

linear

SYN 16-MAR-2000

QY 3266 TTACCGGATACCTGTCGCGCTTTCTCCGTTCCGGAAGCGTGGCGGTTTCTCATAGCTCAC 3325
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 Db 2219 ATCTAGCGGTGTACAGAGTTCTTGAAGTGGTGGCTTAACTACGCTTACACTAGAGAA 2160
 QY 3566 CAGTATTTGTTATCTGCGCTCTGCTGAAGCAGTTACTCTTGGAAAAAGAGTTGTTAGCT 3625
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RESULT 5
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 LOCUS

DEFINITION
 Cloning vector pKIL119 ccdB gene, complete cds and
 kanamycin-resistance gene (Km^r) gene fragment.

ACCESSION
 L38499

VERSION
 L38499.1

KEYWORDS
 ccdB gene; kanamycin resistance.
 Cloning vector pKIL119

SYNCCDBB 2999 bp DNA linear SYN 16-MAR-2000
 Cloning vector pKIL119 ccdB gene, complete cds and
 kanamycin-resistance gene (Km^r) gene fragment.
 L38499
 L38499.1 GI:986979
 ccdB gene; kanamycin resistance.
 Cloning vector pKIL119

ORGANISM Cloning vector pKIL119
artificial sequences; vectors.
REFERENCE 1 (bases 1 to 2999)
AUTHORS Bernard, P.
TITLE New ccdB positive-selection cloning vectors with kanamycin or chloramphenicol selectable markers
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Matches 2359; Conservative 0; Mismatches 26; Indels 146; Gaps 2;

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VERSION AY189829.1 GI:28435539
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ORGANISM artificial sequences; vectors.
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AUTHORS Lee,D.W., Haag,J.R. and Aramayo,R.
TITLE Construction of strains for rapid homokaryon purification after integration of constructs at the histidine-3 (his-3) locus of Neurospora crassa
JOURNAL Curr. Genet. 43 (1), 17-23 (2003)
PUBMED 12684841
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VERSION
AY222815.1
KEYWORDS
Cloning vector pK19mob2
Cloning vector pK19mob2
artificial sequences; vectors.
SOURCE
Kirchner, O. and Tauch, A.
ORGANISM
1 (bases 1 to 3036)
REFERENCE
Kirchner, O. and Tauch, A.
AUTHORS
Tools for genetic engineering in the amino acid-producing bacterium
Corynebacterium glutamicum
J. Biotechnol. 104 (1-3), 287-299 (2003)
JOURNAL
MEDLINE
22830032
PUBMED
12948646
REFERENCE
2 (bases 1 to 3036)
AUTHORS
Kirchner, O. and Tauch, A.
TITLE
Direct Submission
Submitted (22-JAN-2003) Department of Genetics, University of
Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
JOURNAL
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LOCUS

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DEFINITION Cloning vector pK19MECA2, complete sequence.

ACCESSION AY219859

VERSION AY219859.1 GI:29164979

KEYWORDS

SOURCE Cloning vector pK19MECA2

ORGANISM Cloning vector pK19MECA2

artificial sequences; vectors.

REFERENCE

1 (bases 1 to 3210)

Kirchner O. and Tauch, A.

Tools for genetic engineering in the amino acid-producing bacterium

Corynebacterium glutamicum

J. Biotechnol. 104 (1-3), 287-299 (2003)

JOURNAL 22830032

MEDLINE 12948646

PUBMED 12948646

REFERENCE

2 (bases 1 to 3210)

Kirchner O. and Tauch, A.

Direct Submission

Submitted (15-JAN-2003)

Department of Genetics, University of

Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany

Location/Qualifiers

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ORIGIN

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VERSION AY222822.1
KEYWORDS
SOURCE
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REFERENCE
AUTHORS Kirchner,O. and Tauch,A.
TITLE Tools for genetic engineering in the amino acid-producing bacterium
Corynebacterium glutamicum
JOURNAL Biotechnol. 104 (1-3), 287-299 (2003)
MEDLINE 22830032
PubMed 12948646
REFERENCE
AUTHORS Kirchner,O. and Tauch,A.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-2003) Department of Genetics, University of
Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
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ACCESSION	AY219861			
VERSION	AY219861.1	GT:29164983		

KEYWORDS Shuttle vector pEC-K19MECA2
SOURCE Shuttle vector pEC-K19MECA2
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 5869)
AUTHORS Kirchner,O. and Tauch,A.
TITLE Tools for genetic engineering in the amino acid-producing bacterium
Corynebacterium glutamicum
J. Biotechnol. 104 (1-3), 287-299 (2003)
MEDLINE 22830032
PUBMED 12948646
REFERENCE 2 (bases 1 to 5869)
AUTHORS Kirchner,O. and Tauch,A.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-2003) Department of Genetics, University of
Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
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Best Local Similarity 86.7%; Pred. No. 0;
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	Matches 2433; Conservative 0; Mismatches 140; Indels 231; Gaps 3;	
QY	2711 CGTAATCATGTCATAGCTGTTTCCTGTGGAATTTGTTATCCGCTCACAATTCACACA 2770	
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Db		
QY	2771 ACATACGAGCCGGAAGCATAAAGTGAAGCCCTGGGGTGCTTAATGAGTGAGCTAACTCA 2830	
Db		
QY	5417 ACATACGAGCCGGAAGCATAAAGTGAAGCCCTGGGGTGCTTAATGAGTGAGCTAACTCA 5358	
Db		
QY	2831 CATTAATTGGTTGGCTCATCTCCCGCTTTCAGTCGGGAAACCTGTGTCGACAGCTGC 2890	
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QY	5357 CATTAATTGGTTGGCTCATCTCCCGCTTTCAGTCGGGAAACCTGTGTCGACAGCTGC 5298	
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Db	4217	CACTGTCCCTTATTCGCACCTTGGCGGTGCTCAACGGGAATCTGCTCTCGCGAGCTGGCC	4158	Db	3137	CCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTGTGGCCAGTCAATAGCCGAATAG	3078
Qy	3903	GAACCTCCG-----GAGTCTGTCCAGCCTCAGGAGCAGTGAACCAACTCG	3949	Qy	4880	CCTCTCCACCAAGCGCGGAGAACCTTGGTGAATCAATCTTGTCAATCATGCGAAA	4939
Db	4157	GGCTACCGCGCGGTAAACAGATGAGGCGAAGCGGTGCTGATGAACCAACCAACAG	4098	Db	3077	CCTCTCCACCAAGCGCGGAGAACCTTGGTGAATCAATCTTGTCAATCATGCGAAA	3018
Qy	3950	CGAGGGGATCGAGCCCGGGTGGGCGAAGAACTCCAGCAGTGAATCCCGCCTCGAGGA	4009	Qy	4940	CGATCCTCATCTCTCTCTTGTATCAGATCTTGTATCCCTTGGCCCATCAGATCCTTGGCGG	4999
Db	4097	GAAGGGCAGCCCACTATCAAGGTGTACTGCTTCCAGACGAAACGAAGAGCGATTGAGGA	4038	Db	3017	CGATCCTCATCTCTCTCTTGTATCAGATCTTGTATCCCTTGGCCCATCAGATCCTTGGCGG	2958
Qy	4010	TCATCCAG-----	4018	Qy	5000	CAAGAAAGCCATCCAGTTTACTTTGCGAGGCTTCCCACTTACAGAGGGCGCCCGCAG	5059
Db	4037	AAAGGGCGCGCGCGGCATGAGCCTGTGCGCTTACCTGTGGCGGTGCGCGAGGGCTA	3978	Db	2957	CAAGAAAGCCATCCAGTTTACTTTGCGAGGCTTCCCACTTACAGAGGGCGCCCGCAG	2898
Qy	4019	-----CGGCGTCCCGGAAACGATTTC	4039	Qy	5060	TGCGAATTCGGTTCGTTGTGTCCATAAAACCGCCAGTCTAGTCTATCGCATGTAAG	5119
Db	3977	CAAAATCACGGGCTCGTGGACTATGAGCAGCTCCGCGAGGGCGTCCCGGAAACGATTTC	3918	Db	2897	TGGCAATTCGGTTCGTTGTGTCCATAAAACCGCCAGTCTAGTCTATCGCATGTAAG	2838
Qy	4040	CGAAGCCCAACCTTTCATGAGAGCGCGGTGAATCGAAATCTCGTATGGCAGCTTGG	4099	Qy	5120	CCCACTGCAAGTACCTGCTTCTTTCGCGTGGTTCCTTTCCTTGTCCAGATAGCCCA	5179
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Qy	4100	GGTCTGCTTGTGCTGCTTTCGAACCCAGAGTCCCGCTCAGAGAACTCGTCAAGAAG	4159	Qy	5180	GTAGTGAATTCATTCACCGGGTTCAGCACCGTTCCTCGGACTGGCTTCTACGTGTTCGG	5239
Db	3857	GGTCTGCTTGTGCTGCTTTCGAACCCAGAGTCCCGCTCAGAGAACTCGTCAAGAAG	3798	Db	2777	GTAGTGAATTCATTCACCGGGTTCAGCACCGTTCCTCGGACTGGCTTCTACGTGTTCGG	2718
Qy	4160	GCATAGAGCGCATGCGTCCGAATCGGAGCGGCGATACCGTAAAGCAGGAGGAGCG	4219	Qy	5240	CTTCTTTAGAGCCCTTGGCGCTGAGTCTTGGCGAGCGTG	5283
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Qy	4220	GTGAGCCATTCGCGCAAGCTTTCAGCAATATCAGGGTAGCCACCTATGTCCTG	4279	RESULT 14			
Db	3737	GTGAGCCATTCGCGCAAGCTTTCAGCAATATCAGGGTAGCCACCTATGTCCTG	3678	LOCUS	AY222814	3035 bp DNA circular SYN 01-OCT-2003	
Qy	4280	ATAGCGTCCGACACCGCGCCAGTTCGATGAATCCAGAAAGCGGCATTTTC	4339	DEFINITION	Cloning vector pK18mob2, complete sequence.		
Db	3677	ATAGCGTCCGACACCGCGCCAGTTCGATGAATCCAGAAAGCGGCATTTTC	3618	ACCESSION	AY222814		
Qy	4340	CACATCATATTCGGCAAGCAGGCATCGCCATGGGTCCAGCAGAGATCTCGCGTCCGG	4399	VERSION	AY222814.1	GI:29242887	
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Qy	4400	CATCGCGCTTGTAGCTGGCGAAGTTCGCTGGCGGAGCCCTGATGCTTTCGTC	4459	SOURCE	Cloning vector pK18mob2		
Db	3557	CATCGCGCTTGTAGCTGGCGAAGTTCGCTGGCGGAGCCCTGATGCTTTCGTC	3498	ORGANISM	Cloning vector pK18mob2		
Qy	4460	CAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTCTCGCTCGATGCGATG	4519	REFERENCE	1 (bases 1 to 3035)		
Db	3497	CAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTCTCGCTCGATGCGATG	3438	AUTHORS	2 (bases 1 to 3035)		
Qy	4520	TTTTCGCTTGTGTGATGGCGAGGTAGCCGATCAAGCGTATGCGAGCCCGCATTCG	4579	TITLE	Tools for genetic engineering in the amino acid-producing bacterium		
Db	3437	TTTTCGCTTGTGTGATGGCGAGGTAGCCGATCAAGCGTATGCGAGCCCGCATTCG	3378		Corynebacterium glutamicum		
Qy	4580	ATGAGCATGATGATATCTTCTCGGAGGAGCAAGGTGAGTACAGAGATCTCGTCC	4639	JOURNAL	U. Biotechnol. 104 (1-3), 287-299 (2003)		
Db	3377	ATGAGCATGATGATATCTTCTCGGAGGAGCAAGGTGAGTACAGAGATCTCGTCC	3318	MEDLINE	22830032		
Qy	4640	CGGCATCTCGCCCAATAGCAGCAGTCCCTTCCGCTTCAGTGAACAAGTCCGAGCAGC	4699	PUBMED	12948646		
Db	3317	CGGCATCTCGCCCAATAGCAGCAGTCCCTTCCGCTTCAGTGAACAAGTCCGAGCAGC	3258	REFERENCE	3 (bases 1 to 3035)		
Qy	4700	TGCGCAAGGAACGCCGCTGTTGGCAGCAAGATAGCGCGCTGCTGCTGCGATTC	4759	AUTHORS	Kirchner,O. and Tauch,A.		
Db	3257	TGCGCAAGGAACGCCGCTGTTGGCAGCAAGATAGCGCGCTGCTGCTGCGATTC	3198	TITLE	Direct Submission		
Qy	4760	ATTGAGGACCGGACAGTGGTCTTCAAAAAGAACCGGGCGCCCTCGCTGACAG	4819		Submitted (22-JAN-2003) Department of Genetics, University of		
Db	3197	ATTGAGGACCGGACAGTGGTCTTCAAAAAGAACCGGGCGCCCTCGCTGACAG	3138	JOURNAL	Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany		
Qy	4820	CCGGAACACGGCGGCATCAGAGCAGCGATTGTCTGTGTGCCCCAGTCAATAGCCGAATAG	4879	FEATURES	Location/Qualifiers		
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ORIGIN						
Query Match		39.3%; Score 2078; DB 12; Length 3035;				
Best Local Similarity		86.7%; Pred. No. 0;				
Matches 2423; Conservative		0; Mismatches 140; Indels 231; Gaps 3;				
QY	2721	GTCTAGCTGTTTCTGTGTGAATTTGTTATCCGCTCAAAATCCACACATACGAGC	2780	2247	GAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACTAGT	
DB	3027	GTCTAGCTGTTTCTGTGTGAATTTGTTATCCGCTCAAAATCCACACATACGAGC	2968	3561	AAGAACAGTATTGTTGTTATCTGGCTCTGCTGAAGCCAGTTACTTCGGAATAAGAGTTGG	
QY	2781	CGAAGCATAAAGTCTAAAGCTCGGGTGCCTAATGAGTGAGCTAACTACATTAATTGC	2840	2187	AAGGACAGTATTGTTGTTATCTGGCTCTGCTGAAGCCAGTTACTTCGGAATAAGAGTTGG	
DB	2967	CGAAGCATAAAGTCTAAAGCTCGGGTGCCTAATGAGTGAGCTAACTACATTAATTGC	2908	3621	TAGCTCTTCATCCGGCAAAACAAACCCGCTGCTAGCGGTGTTTTTTTTTTGTTGCAAGCA	
QY	2841	GTTGGCTCACTGCGCGCTTTCAGTCGGGAACCTGTCGCCAGCTGCATTAATGAAT	2900	2127	TAGCTCTTCGATCCGGCAAAACAAACCCGCTGCTAGCGGTGTTTTTTTTTTGTTGCAAGCA	
DB	2907	GTTGGCTCACTGCGCGCTTTCAGTCGGGAACCTGTCGCCAGCTGCATTAATGAAT	2848	3681	GCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGTCTTTGATCTTTCTACGGGGTC	
QY	2901	CGGCCAACCGCGGGGAGCGGTTTCGGTATTGGGCGCTCTTCGGCTTCCTGCTCAC	2960	2067	GCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGTCTTTGATCTTTCTACGGGGTC	
DB	2847	CGGCCAACCGCGGGGAGCGGTTTCGGTATTGGGCGCTCTTCGGCTTCCTGCTCAC	2788	3741	TCACGCTCAGTGGAAACGAAACTCAGTTAAGGATTTTGGTTCATGAGATTATCGTCG--	
QY	2961	TGACTCGTGGCTCGGTCGCTCGCGCGAGCGGTATCAGCTCACTCAAGAGCGGT	3020	2007	TGACGCTCAGTGGAAACGAAACTCAGTTAAGGATTTTGGTTCATGAGATTATCGTCG--	
DB	2787	TGACTCGTGGCTCGGTCGCTCGCGCGAGCGGTATCAGCTCACTCAAGAGCGGT	2728	3799	-----	
QY	3021	AATACGGTTATCCACAGATCAGGGGATAACGCAGGAAGAACATGTGAGCAAAAGGCCA	3080	1947	TAACCTCTCTCGGGTCAATTATAGGATTTTTCGGTATATCCATCCCTTTTCGCACGA	
DB	2727	AATACGGTTATCCACAGATCAGGGGATAACGCAGGAAGAACATGTGAGCAAAAGGCCA	2668	3799	-----	
QY	3081	GCAAAAGCCAGGAACCGTAAAGCGCGTTCCTGGCGCTTTTCCATAGGCTCCGCC	3140	1887	TATACAGGATTTTGCACAAAGGGTTCGTGTAGACTTTTCCTTGGTGTATCCAAACGGCGTCA	
DB	2667	GCAAAAGCCAGGAACCGTAAAGCGCGTTCCTGGCGCTTTTCCATAGGCTCCGCC	2608	3799	-----	
QY	3141	CCCTGACGAGCATCACAAAATCAGCGCTCAAGTCAGAGTGGCGAAACCCGACAGGACT	3200	3799	-----	
DB	2607	CCCTGACGAGCATCACAAAATCAGCGCTCAAGTCAGAGTGGCGAAACCCGACAGGACT	2548	1828	TATACAGGATTTTGCACAAAGGGTTCGTGTAGACTTTTCCTTGGTGTATCCAAACGGCGTCA	
QY	3201	ATAAGATACAGGCGTTTCCCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCT	3260	3799	-----	
DB	2547	ATAAGATACAGGCGTTTCCCTGGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCT	2488	3799	-----	
QY	3261	CGCGTTTACCGGATACCTGTCGCGCTTTCCTCTCGGAGCGGTGGCGTTCTCATAG	3320	1587	GCGCGGCGCATGAGCCTGTGCGCCTACCTGCTGCGCGTCCGCGACGGGCTACAAAATCAGG	
DB	2487	CGCGTTTACCGGATACCTGTCGCGCTTTCCTCTCGGAGCGGTGGCGTTCTCATAG	3320	4019	-----	
QY	3321	CTCAGCGTGTAGGTATCTCAGTTTCGGTGTAGTTCGTTCCGCTTCCGCTTCTCTGTTCCGACCT	4049	1527	GCGCGTGGAGACTATGAGCACGTCGCGAGGGCGTCCCGAAAAACGATTCGGAAGCCCAA	
DB	2427	CTCAGCGTGTAGGTATCTCAGTTTCGGTGTAGTTCGTTCCGCTTCCGCTTCTCTGTTCCGACCT	4109	4050	CCCTTTCATAGAGGCGGCTGGAATCGAAATCTCGTATGCGAGTTGGGCGTCCGTTG	
QY	3381	CGAACCCCCGTTACGCCGACCGCTCGCTTATCCGGTAACTATCGTCTTTCGATCCAA	1408	1467	CCCTTTCATAGAGGCGGCGTGGGATCGAAATCTCGTATGCGAGTTGGGCGTCCGTTG	
DB	2367	CGAACCCCCGTTACGCCGACCGCTCGCTTATCCGGTAACTATCGTCTTTCGATCCAA	4169	4110	GTGCGTCAATTTGAAACCCAGAGTCCGCTCAGAAGAACTCGTCAAGAAGCGGATAGAG	
QY	3441	CCCGGTAAGACACGACTTATCGCACTGGCAGAGCCACTGGTAACAGGATTAGCAGGC	1348	4170	GCGATGCCCTCGGATCCGGAGCGCGGATACCGTAAAGCACAGGAAGCGGTACGCCAT	
DB	2307	CCCGGTAAGACACGACTTATCGCACTGGCAGAGCCACTGGTAACAGGATTAGCAGGC	4229	1347	GCGATGCCCTCGGAATCGGGAGCGCGGATACCGCTAAAGCACAGGAAGCGGTACGCCAT	
QY	3501	GAGGTATGTAGGCGGTCTACAGATTCTTGAAATGGTGGCCTTAACTACGGCTACTAGT	1288	4230	TCGCGCCCAAGCTCTTCAGCAATATCACGGGTAGCCAAACGCTATGTCTCTGATAGCGGTCC	
				4289	1287	TCGCGCCCAAGCTCTTCAGCAATATCACGGGTAGCCAAACGCTATGTCTCTGATAGCGGTCC
				1228	4290	GCCACACCCAGCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCACCATGATA
				4349	1227	GCCACACCCAGCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCACCATGATA
				1168	4350	TTCCGCAAGCAGGCGATCCCAATGGGTACGACAGATCTCTCGCGTGGGCGATCGCGCC
				4409	1167	TTCCGCAAGCAGGCGATCCCAATGGGTACGACAGAGATCTCTCGCGTGGGCGATCGCGCC
				1108		

AUTHORS		Tauch, A., Kirchner, O., Löffler, B., Gotker, S., Puhler, A. and Kalinowski, J.	
TITLE		Efficient electrotransformation of <i>Corynebacterium diphtheriae</i> with a mini-replicon derived from the <i>Corynebacterium glutamicum</i> plasmid pGAI	
JOURNAL		Curr. Microbiol. 45 (5), 362-367 (2002)	
MEDLINE		22217619	
PUBMED		12232668	
REFERENCE		2 (bases 1 to 3053)	
AUTHORS		Tauch, A., Kirchner, O., Löffler, B., Gotker, S., Puhler, A. and Kalinowski, J.	
TITLE		Direct Submission	
JOURNAL		Submitted (22-JAN-2003) Department of Genetics, University of Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany	
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ORIGIN	Query Match 39.3%; Score 2078; DB 12; Length 3053;	Best Local Similarity 86.7%; Pred. No. 0;	Matches 2423; Conservative 0; Mismatches 140; Indels 231; Gaps 3;
QY	2721	GTCTAGCTGTTTCTCTGTGTAATTTGTTATCCGCTCACAAATCCACACACATACGAGC	2780
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QY	2781	CGGAAGCATAAAGTGAAGCTGGGGTGCCTAATGAGTGAGCTAACTCACTTAATTTGC	2840
Db	2985	CGGAAGCATAAAGTGAAGCTGGGGTGCCTAATGAGTGAGCTAACTCACTTAATTTGC	2926
QY	2841	GTTCGGCTCACTGCGCGTTTCCAGTCGGGAAACCTGTCTGCGAGCTGCATTAATGAAT	2900
Db	2925	GTTCGGCTCACTGCGCGTTTCCAGTCGGGAAACCTGTCTGCGAGCTGCATTAATGAAT	2866
QY	2901	CGGCCAACGCGCGGGAGAGCGGTTTCGGTATTGGGCGCTCTTCGGCTTCTCGCTCAC	2960
Db	2865	CGGCCAACGCGCGGGAGAGCGGTTTCGGTATTGGGCGCTCTTCGGCTTCTCGCTCAC	2806
QY	2961	TGACTCGCTGCGCTCGGCTTCGGCTCGGCGAGCGGTATCAGTCTCATCTCAAGGCGGT	3020
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QY	3021	AATACGGTTATCCAGAAATCAGGGGATACCGCAGAAAGACATGTGAGCAAAAGGCCA	3080
Db	2745	AATACGGTTATCCAGAAATCAGGGGATACCGCAGAAAGACATGTGAGCAAAAGGCCA	2686
QY	3081	GCAAAAGGCCAGAACCGTAAAGGCGCGTTGTGCGGTTTTCCTATAGGCTCCGCC	3140
Db	2685	GCAAAAGGCCAGAACCGTAAAGGCGCGTTGTGCGGTTTTCCTATAGGCTCCGCC	2626

QY	3141	CCCTGACGAGCATCACAAATCGACGCTCAAGTCAGAGGTGGCGGAAAACCCGACAGGACT	3200	Db	1545	GGCGTCGTGGACTATGAGCACGTCCTCCGAGGGGCTCCCGGAAAAAGTTCGGAAGGCCAA	1486
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QY	3201	ATAAAGATACCAAGGGTTTCCCGCTGGAAAGTCCCTTCGTCGCTCTCCCTGTTCCGACCCCT	3260	Db	1485	CTTTTCATAGAAAGGGGGGGTGGAAATCTCGTGTATGGCAGGTTGGGGGTTCGCTTG	1426
Db	2565	ATAAAGATACCAAGGGTTTCCCGCTGGAAAGTCCCTTCGTCGCTCTCCCTGTTCCGACCCCT	2506	QY	4110	GTCCGTCTATTTCGAACCCGAGAGTCCGCTCAGAAAGTCTCGTCAAGAAGGGGATAGAAG	4169
QY	3261	GGCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAG	3320	Db	1425	GTCCGTCTATTTCGAACCCGAGAGTCCGCTCAGAAAGTCTCGTCAAGAAGGGGATAGAAG	1366
Db	2505	GGCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAG	2446	QY	4170	GGCATGCGCTCGGAATTCGGAGCGGCGATACCGTAAAGCACGAGAAGCGGTTCAGCCAT	4229
QY	3321	CTCAGCGTGTAGGTATCTCAGTTCGGTGTAGTTCGCTCAAGCTGGGCTGTGTGCA	3380	Db	1365	GGCATGCGCTCGGAATTCGGAGCGGCGATACCGTAAAGCACGAGAAGCGGTTCAGCCAT	1306
Db	2445	CTCAGCGTGTAGGTATCTCAGTTCGGTGTAGTTCGCTCAAGCTGGGCTGTGTGCA	2386	QY	4230	TGCGCGCCAAAGTCTTCAGCAATATCAGGGTAGCCAAAGTATGTCCTGTATAGCGGTCC	4289
QY	3381	CGAACCCCGCTTACGCCGACCGCTGCGCTTATCCGCTAACTATCGTCTGAGTCCAA	3440	Db	1305	TGCGCGCCAAAGTCTTCAGCAATATCAGGGTAGCCAAAGTATGTCCTGTATAGCGGTCC	1246
Db	2385	CGAACCCCGCTTACGCCGACCGCTGCGCTTATCCGCTAACTATCGTCTGAGTCCAA	2326	QY	4290	GCCACACCCAGCGGCCACAGTTCGATGAATCCAGAAAAGCGCCATTTCCACCATGATA	4349
QY	3441	CCCGTAAAGACAGCACTTATCGCCACTGCGACGACCCACTGTAACAGGATTTAGCAGAC	3500	Db	1245	GCCACACCCAGCGGCCACAGTTCGATGAATCCAGAAAAGCGGCCATTTTCACCATGATA	1186
Db	2325	CCCGTAAAGACAGCACTTATCGCCACTGCGACGACCCACTGTAACAGGATTTAGCAGAC	2266	QY	4350	TTCGCAAGCAGGCGATCCCATGCGGTTCACGACGAGATCCTCGCGTCGCGCATCGCGCC	4409
QY	3501	GAGGTATGTAGCGGTGTACAGAGTCTTGAAGTGTGGCTTAACAGGCTACACTAG	3560	Db	1185	TTCGCAAGCAGGCGATCCCATGCGGTTCACGACGAGATCCTCGCGTCGCGCATCGCGCC	1126
Db	2265	GAGGTATGTAGCGGTGTACAGAGTCTTGAAGTGTGGCTTAACAGGCTACACTAG	2206	QY	4410	TTGAGCCTTGGGCAACAGTTCGGCTGGCGCGAGCCCTGATGCTTCTTCGATCAGATCATCC	4469
QY	3561	AAGAACAGTATTGATCTCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGG	3620	Db	1125	TTGAGCCTTGGGCAACAGTTCGGCTGGCGCGAGCCCTGATGCTTCTTCGATCAGATCATCC	1066
Db	2205	AAGAACAGTATTGATCTCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGG	2146	QY	4470	TGATCGACAAGACCGGCTTCATCCGAGTACGTCCTCGATCGATCGATGTTTCGCTTGG	4529
QY	3621	TAGCTCTTGATCCGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCA	3680	Db	1065	TGATCGACAAGACCGGCTTCATCCGAGTACGTCCTCGATCGATCGATGTTTCGCTTGG	1006
Db	2145	TAGCTCTTGATCCGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCA	2086	QY	4530	TGTCGAATGGCGAGGTAGCCGATCAAGCGTATGACGCCCGCATTCATTCAGCCATG	4589
QY	3681	GCAGATTACGCGCAGAAAAGAGTCTCAGAGAGATCCCTTGATCTTTCACGGGTC	3740	Db	1005	TGTCGAATGGCGAGGTAGCCGATCAAGCGTATGACGCCCGCATTCATTCAGCCATG	946
Db	2085	GCAGATTACGCGCAGAAAAGAGTCTCAGAGAGATCCCTTGATCTTTCACGGGTC	2026	QY	4590	ATGATATCTTCTCGGAGGAGCAAGGTAGATGACGAGAGATCTTCGCCCGCATTCG	4649
QY	3741	TGACGCTCAGTGGAAACAACTCACGTTAAGGATTTTGTCATGAGATTATCGTCG	3798	Db	945	ATGATATCTTCTCGGAGGAGCAAGGTAGATGACGAGAGATCTTCGCCCGCATTCG	886
Db	2025	TGACGCTCAGTGGAAACAACTCACGTTAAGGATTTTGTCATGAGATTATCGTCG	1966	QY	4650	CCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGAACAGTTCGAGCAGAGTTCGCGCAAGGA	4709
QY	3799	-----	3798	Db	885	CCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGAACAGTTCGAGCAGAGTTCGCGCAAGGA	826
Db	1965	TAACCTGCTTCGGGGTCAATTATAGCGAATTTTTCGGTATATCCATCCTTTTCGCA	1906	QY	4710	ACGCCCTGCTGGCCAGCCACGATAGCGGCTGCTGCTCCTCGATTCATTCAGGGCA	4769
QY	3799	-----	3798	Db	825	ACGCCCTGCTGGCCAGCCACGATAGCGGCTGCTGCTCCTCGATTCATTCAGGGCA	766
Db	1905	TATACAGATTTCCAAAGGGTTCGTAGACTTTTCCTTGGTGTATCCAAAGCGGTCA	1846	QY	4770	CCGACAGGTTCGCTTTGACAAAAGAACCGGGCGCCCTTCGCTGACAGCGGAAACAG	4829
QY	3799	-----	3852	Db	765	CCGACAGGTTCGCTTTGACAAAAGAACCGGGCGCCCTTCGCTGACAGCGGAAACAG	706
Db	1845	CGGGCAGGATAGTGAAGTAGGCCACCCGCGAGCGGTTCCTTCTTCAGTCCCT	1786	QY	4830	CGGCAATCAGACAGCCGATTTGCTGTTCGCCAGTCATAGCGGATAGCTTCACCC	4889
QY	3853	GGATAGCGCTGCTGTGTTCTGTAAGCCGAGGATTTGCACTGCGGTAGAACTCCGC	3911	Db	705	CGGCAATCAGACAGCCGATTTGCTGTTCGCCAGTCATAGCGGATAGCTTCACCC	646
Db	1785	TATTCGACCTGCGGTGCTCAACGGGAATCCTGCTCTGCGAGGCTGCGCGGTACCGCC	1726	QY	4890	CAAGCGCCCGGAAACCTGCGTCAATTCATTTGTTCAATTCATTCGCAACGATTCCTCAT	4949
QY	3912	-----	3959	Db	645	CAAGCGCCCGGAAACCTGCGTCAATTCATTTGTTCAATTCATTCGCAACGATTCCTCAT	586
Db	1725	GGCGTAACAGATGAGGCAACGGATGGCTGATGAACCAAGCCACAGAGAGGCGAGC	1666	QY	4950	CTGTCTCTTGTATCAGATCTTGTATCCCTCGCGCATCAGATCCTTGGCGGCAAGAGCC	5009
QY	3960	GAGCCCGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATTCATCCAGC	4018	Db	585	CTGTCTCTTGTATCAGATCTTGTATCCCTCGCGCATCAGATCCTTGGCGGCAAGAGCC	526
Db	1665	CCACCTATCAAGGTGTACTGCTTCCAGACGACAGAGGATGAGGAAAAGCGGCG	1606	QY	5010	ATCCAGTTTACTTTGACAGGCTTCCCAAACCTTACAGAGGCGCCCGCTGCGCAATTC	5069
QY	4019	-----	4018	Db	525	ATCCAGTTTACTTTGAGGGCTTCCCAAACCTTACAGAGGCGCCCGCTGCGCAATTC	466
Db	1605	CGCGCCGCGCATGAGCCTGTGCGCTACCTGTGCGCGTCGCGCAGGCTACAAAATCAG	1546	QY	5070	GGTTCGCTTGTCTCCATAAAACCGCCAGTCTAGCTATCGCATGTAAAGCCACATGCAA	5129
QY	4019	-----	4049				

Db 465 GGTTCGCTTGCTGTCATATAACCGCCAGTCTAGCTATCGCCATGTAAAGCCCACTGCAA 406
QY 5130 GCTACCTGCTTCTCTCTTTGCGCTTGGCTTTTCCCTTGTCCAGATAGCCCAAGTAGCTGACA 5189
Db 405 GCTACCTGCTTCTCTCTTTGCGCTTGGCTTTTCCCTTGTCCAGATAGCCCAAGTAGCTGACA 346
QY 5190 TTCATCCGGGTCAGACCCGTTTCTCGGACTGGCTTTCTACGTGTTCGGCTTCCTTTAG 5249
Db 345 TTCATCCGGGTCAGACCCGTTTCTCGGACTGGCTTTCTACGTGTTCGGCTTCCTTTAG 286
QY 5250 CAGCCCTTGGCCCTGAGTGTCTGCGGACGCGTG 5283
Db 285 CAGCCCTTGGCCCTGAGTGTCTGCGGACGCGTG 252

Search completed: August 4, 2004, 11:02:29
Job time : 19782 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 01:48:34 ; Search time 1848 Seconds
(without alignments)
12144.605 Million cell updates/sec

Title: US-09-921-143-36

Perfect score: 5283

Sequence: 1 aagcttgacattatgcgact.....tgagtcttgcgcagcgtg 5283

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_29Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5283	100.0	5283	6	ABK10062 Expressio
2	2240	42.4	8349	3	AAAL5565 pMON30464
3	2017.2	38.2	6136	2	AAV29673 Hybrid NA
4	1793.4	33.9	4800	2	AAV52020 Synthetic
5	1652.4	31.3	5594	2	AAV33629 GENSA 981
6	1634.4	30.9	5285	4	AAH74865 Nucleotid
7	1632.8	30.9	5285	7	ABX94355 Rolling c
8	1618.2	30.6	6561	2	AAV33630 Plasmid V
9	1603.8	30.4	2192	6	ABQ78294 Nucleotid
10	1603.8	30.4	3534	6	ABQ78293 Nucleotid
11	1603.8	30.4	3534	8	AAAL62060 TV-GHRH p
12	1603.8	30.4	3534	8	AAAL62062 Wild-type
13	1603.8	30.4	3534	8	AAAL62059 TI-GHRH p
14	1603.8	30.4	3534	8	AAAL62058 PSP-HV-GH
15	1603.8	30.4	3534	8	AAAL62061 15/27/28-
16	1603.8	30.4	3534	8	AAAL60444 TI-GHRH p
17	1603.8	30.4	3534	8	AAAL60445 TV-GHRH p
18	1603.8	30.4	3534	8	AAAL60446 15/27/28
19	1603.8	30.4	3534	8	AAAL60443 pSP-HV-GH
20	1603.8	30.4	3534	8	AAAL60447 Wild-type
21	1603.8	30.4	3534	9	ACF04661 Wildtype
22	1603.8	30.4	3534	9	ACF04660 15/27/28
23	1603.8	30.4	3534	9	ACF04657 HV-GHRH o

24	1603.8	30.4	3534	9	ACF04659	ACF04659 TV-GHRH o
25	1603.8	30.4	3534	9	ACF04658	ACF04658 TI-GHRH o
26	1603.8	30.4	3599	2	AAV50428	AAV50428 Plasmid p
27	1603.8	30.4	3599	2	AAV40796	AAV40796 Actual se
28	1603.4	30.4	3558	8	AAAL60457	AAAL60457 pGR1774 p
29	1602.2	30.3	3600	2	AAV50427	AAV50427 Plasmid p
30	1602.2	30.3	3600	2	AAV40795	AAV40795 Expected
31	1602.2	30.3	5707	2	AAV88055	AAV88055 Plasmid p
32	1600	30.3	5966	2	AAZ40417	AAZ40417 Plasmid p
33	1571.6	29.7	4685	4	AAAF30342	AAAF30342 Construct
34	1570.8	29.7	5068	2	AAAH4027	AAAH4027 MMP9 prom
35	1570	29.7	4517	5	AAAH24427	AAAH24427 PBKCMV ph
36	1570	29.7	4518	2	AAV33626	AAV33626 Plasmid p
37	1570	29.7	4775	8	ACC84214	ACC84214 C-kit tar
38	1570	29.7	4886	6	AAAD42469	AAAD42469 Human aeq
39	1570	29.7	4886	7	ACA61962	ACA61962 Aequorin
40	1570	29.7	5031	2	AAZ25355	AAZ25355 EGFP/DRM
41	1570	29.7	5054	2	AAZ25354	AAZ25354 EGFP/DRM
42	1570	29.7	5130	2	AAZ25353	AAZ25353 EGFP/DRM
43	1570	29.7	5168	2	AAZ25351	AAZ25351 EGFP/DRM
44	1570	29.7	5619	3	AAA07773	AAA07773 DNA seque
45	1570	29.7	5627	3	AAA07778	AAA07778 DNA seque

ALIGNMENTS

RESULT 1
ABK10062
ID ABK10062 standard; DNA; 5283 BP.
XX
AC ABK10062;
XX
DT 21-MAY-2002 (first entry)
XX
DE Expression vector construct pVGI.1 containing VEGF-2 insert.
XX
KW Human; vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1;
KW chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; pHE4a;
KW allergic reaction; organ rejection; inflammatory condition; arrhythmia;
KW hyperproliferative disorder; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cardiovascular disorder; embolism;
KW heart valve disease; aneurysm; arterial occlusive disorder; gene therapy.
XX
OS Synthetic.
XX
DN WO200211769-A1.
XX
PD 14-FEB-2002.
XX
PF 03-AUG-2001; 2001WO-US024658.
XX
PR 04-AUG-2000; 2000US-0223276P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Coleman TA;
XX
WPI 2002-217153/27.
XX
PT Isolated nucleic acid having expression vector construct with vascular
PT endothelial growth factor-2 insert, useful for treating chronic limb
PT ischemia or myocardial ischemia, autoimmune disorders and allergic
PT conditions.
XX
PS Disclosure; Fig 31; 241bp; English.
XX
CC The invention relates to an isolated nucleic acid comprising pVGI.1
CC expression vector construct containing the vascular endothelial growth
CC factor 2 (VEGF-2) insert. The nucleic acid is useful for producing a host
CC cell by transducing, transforming or transfecting a host cell with the
CC DNA and for treating a patient having chronic limb ischaemia or
CC myocardial ischaemia, or a disease or disorder selected from autoimmune

CC disorders (e.g. rheumatoid arthritis, dermatitis), allergic reactions or
CC conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g.
CC Crohn's disease), hyperproliferative disorders (e.g. Gaucher's disease),
CC diseases due to viral, bacterial, fungal or parasitic infection,
CC cardiovascular disorders (e.g. cardiomyopathy), arrhythmia, heart valve
CC diseases, aneurysms, arterial occlusive disorders and embolism. This
CC sequence represents the pVGI.1 expression vector containing the VEGF-2
CC insert
XX
SQ Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 U; 0 Other;
Query Match 100.0%; Score 5283; DB 6; Length 5283;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCTTGACCTTATCGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTAT 60
DB 1 AAGCTTGACCTTATCGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTAT 60
QY 61 TACCATGGTGATGCGGTTTGGCAGTACATCAATGCGGTGATAGCGGTTTGAATCAGC 120
DB 61 TACCATGGTGATGCGGTTTGGCAGTACATCAATGCGGTGATAGCGGTTTGAATCAGC 120
QY 121 GGGATTCCAGTCTCCACCCCACTGAGTCAATGGAGTTTGTGTCACCAAAATCA 180
DB 121 GGGATTCCAGTCTCCACCCCACTGAGTCAATGGAGTTTGTGTCACCAAAATCA 180
QY 181 ACGAGACTTTCAAAATGTCGTAACTCCGCCCATTTAGCGCAAAATGGCGGTAGGCG 240
DB 181 ACGAGACTTTCAAAATGTCGTAACTCCGCCCATTTAGCGCAAAATGGCGGTAGGCG 240
QY 241 AACATGCTTATGACGGTGAGTGTAGCAACATGCGCTTATAGGAGAGAAAGCCCGTG 300
DB 241 AACATGCTTATGACGGTGAGTGTAGCAACATGCGCTTATAGGAGAGAAAGCCCGTG 300
QY 301 CATGCGGTTGTGGGAGTAAAGTGATGATGCTGGTATGATGCTGTCCTTGTAGGAAG 360
DB 301 CATGCGGTTGTGGGAGTAAAGTGATGATGCTGGTATGATGCTGTCCTTGTAGGAAG 360
QY 361 GCAACAGACGGGTCTTAACACGGATTGGACGAACCACTCGAATTCGCAATTCGAGATATT 420
DB 361 GCAACAGACGGGTCTTAACACGGATTGGACGAACCACTCGAATTCGCAATTCGAGATATT 420
QY 421 GTATTAAAGTCCAGCTCGATCAATAAAGCGCATTTGACCATTCACACATTTGATG 480
DB 421 GTATTAAAGTCCAGCTCGATCAATAAAGCGCATTTGACCATTCACACATTTGATG 480
QY 481 CACCTGGGTTGGATCGATCCATCATGCTGGGCTTCTCTCTGTCGCTGTTCT 540
DB 481 CACCTGGGTTGGATCGATCCATCATGCTGGGCTTCTCTCTGTCGCTGTTCT 540
QY 541 CTGCTGCGGCTGCGCTGCTCCGGGTCTTCGAGGCGCGCGCGCGCGCGCGCTTC 600
DB 541 CTGCTGCGGCTGCGCTGCTCCGGGTCTTCGAGGCGCGCGCGCGCGCGCGCTTC 600
QY 601 GAGTCGGGACTGACCTCTCGACCGGAGCCGAGCGGGTACGCGCGCTTATGCA 660
DB 601 GAGTCGGGACTGACCTCTCGACCGGAGCCGAGCGGGTACGCGCGCTTATGCA 660
QY 661 AGCAAGATCTGGAGGAGCAGTTACGCTGCTGTCAGTGTAGATGAATCATGACTGTA 720
DB 661 AGCAAGATCTGGAGGAGCAGTTACGCTGCTGTCAGTGTAGATGAATCATGACTGTA 720
QY 721 CTCTACCCAGAAATTTGGAAATGTACAAGTGTACGCTAAGAAAGAGCGCTGGCAAT 780
DB 721 CTCTACCCAGAAATTTGGAAATGTACAAGTGTACGCTAAGAAAGAGCGCTGGCAAT 780
QY 781 AACAGAGACAGCCCACTCTCACTCAAGACAGAGAGACTATAAAATTTGTCGAGCA 840
DB 781 AACAGAGACAGCCCACTCTCACTCAAGACAGAGAGACTATAAAATTTGTCGAGCA 840
QY 841 CATTATAATACAGAGATCTTGAAGATTTGTAATGAGTGGAGAAAGACTCAATGCATG 900
DB 841 CATTATAATACAGAGATCTTGAAGATTTGTAATGAGTGGAGAAAGACTCAATGCATG 900
QY 901 CCACGGAGGTGTGTATAGATGTGGGGAAGAGATTGAGTCGCCACAAAACACCTTCTTT 960
DB 901 CCACGGAGGTGTGTATAGATGTGGGGAAGAGATTGAGTCGCCACAAAACACCTTCTTT 960
QY 961 AAACCTCCATGTGTCCGTCTACAGATGTGGGGTGTGCTCAATAGTAGGGGGTGCAG 1020
DB 961 AAACCTCCATGTGTCCGTCTACAGATGTGGGGTGTGCTCAATAGTAGGGGGTGCAG 1020
QY 1021 TGCATGAACCAACAGCAACGAGCTTACCTCAGCAAGAGCTTATTTGAAATTTACAGTGCCTC 1080
DB 1021 TGCATGAACCAACAGCAACGAGCTTACCTCAGCAAGAGCTTATTTGAAATTTACAGTGCCTC 1080
QY 1081 TCTCAAGGCCCAACACAGTAAACATGATTTGCAATCACACTTCTGCCGATGATG 1140
DB 1081 TCTCAAGGCCCAACACAGTAAACATGATTTGCAATCACACTTCTGCCGATGATG 1140
QY 1141 TCTAAACTGGATGTTTACAGACAAGTTCATTTTATTTAGACGTTTCCCTGCCAGCAACA 1200
DB 1141 TCTAAACTGGATGTTTACAGACAAGTTCATTTTATTTAGACGTTTCCCTGCCAGCAACA 1200
QY 1201 CTACCAAGTGTACGGCAGCAACAGACCTGCCCAACCAATTTACATGTGGAATTAATCAC 1260
DB 1201 CTACCAAGTGTACGGCAGCAACAGACCTGCCCAACCAATTTACATGTGGAATTAATCAC 1260
QY 1261 ATCTCAGATGCTCGCTCAGGAAGATTTATGTTTTCTCGATGCTGAGATGACTCA 1320
DB 1261 ATCTCAGATGCTCGCTCAGGAAGATTTATGTTTTCTCGATGCTGAGATGACTCA 1320
QY 1321 ACAGATGGAATTCATCTGTGGAACCAACAGGAGCTGGATGAAGAGACCTGTGAG 1380
DB 1321 ACAGATGGAATTCATCTGTGGAACCAACAGGAGCTGGATGAAGAGACCTGTGAG 1380
QY 1381 TGTGCTGCAGAGCGGGCTTCGGCTGCGAGTGTGACCAACCAACCAACCAACCAACCA 1440
DB 1381 TGTGCTGCAGAGCGGGCTTCGGCTGCGAGTGTGACCAACCAACCAACCAACCAACCA 1440
QY 1441 AACTCATGCGAGTGTGCTGTAAACCAACCTTCCCGAGCAATGTGGGGCAACCGA 1500
DB 1441 AACTCATGCGAGTGTGCTGTAAACCAACCTTCCCGAGCAATGTGGGGCAACCGA 1500
QY 1501 GAATTTGATGAAAAACACATGCCAGTGTGTATGTAAAGAACCTGCCCGCAACCAACCC 1560
DB 1501 GAATTTGATGAAAAACACATGCCAGTGTGTATGTAAAGAACCTGCCCGCAACCAACCC 1560
QY 1561 CTAAATCTGGAAAAATGTGCTGTGAATGTACAGAAAGTCCACAGAAATGCTTTGTTAAA 1620
DB 1561 CTAAATCTGGAAAAATGTGCTGTGAATGTACAGAAAGTCCACAGAAATGCTTTGTTAAA 1620
QY 1621 GGAAGAAAGTCCACCAACCAACATGCACTGTTCAGACGGCATGTACGAACCGCCAG 1680
DB 1621 GGAAGAAAGTCCACCAACCAACATGCACTGTTCAGACGGCATGTACGAACCGCCAG 1680
QY 1681 AAGGCTTGTGAGCCAGGATTTTATATAGTGAAGAGTGTGTGTTGTGCTTCAATAT 1740
DB 1681 AAGGCTTGTGAGCCAGGATTTTATATAGTGAAGAGTGTGTGTTGTGCTTCAATAT 1740
QY 1741 TGGAAAAAGCAACCAATGAGCTTAATCTAGGATCCGTACCGTCCCGAGCTTTTGTCAAAC 1800
DB 1741 TGGAAAAAGCAACCAATGAGCTTAATCTAGGATCCGTACCGTCCCGAGCTTTTGTCAAAC 1800
QY 1801 AGCACCTTTGTGTTCTTCACTTGGTGAAGCTCTCTACCTGTGTGTGGGAGCGCTGGAT 1860
DB 1801 AGCACCTTTGTGTTCTTCACTTGGTGAAGCTCTCTACCTGTGTGTGGGAGCGCTGGAT 1860
QY 1861 TCTTCTACACACCATGTCCCGCGGAGAGTGGAGACCAACAGTAAAGCTTGTCTCT 1920
DB 1861 TCTTCTACACACCATGTCCCGCGGAGAGTGGAGACCAACAGTAAAGCTTGTCTCT 1920
QY 1921 GAATTTCTATCCCAAGTCTTACCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1980
DB 1921 GAATTTCTATCCCAAGTCTTACCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1980

841 CATTATAATACAGAGATCTTGAAGATTTGATATAGTGGAGAAAGACTCAATGCATG 900
901 CCACGGAGGTGTGTATAGATGTGGGGAAGAGATTGAGTCGCCACAAAACACCTTCTTT 960
901 CCACGGAGGTGTGTATAGATGTGGGGAAGAGATTGAGTCGCCACAAAACACCTTCTTT 960
961 AAACCTCCATGTGTCCGTCTACAGATGTGGGGTGTGCTCAATAGTAGGGGGTGCAG 1020
961 AAACCTCCATGTGTCCGTCTACAGATGTGGGGTGTGCTCAATAGTAGGGGGTGCAG 1020
1021 TGCATGAACCAACAGCAACGAGCTTACCTCAGCAAGAGCTTATTTGAAATTTACAGTGCCTC 1080
1021 TGCATGAACCAACAGCAACGAGCTTACCTCAGCAAGAGCTTATTTGAAATTTACAGTGCCTC 1080
1081 TCTCAAGGCCCAACACAGTAAACATGATTTGCAATCACACTTCTGCCGATGATG 1140
1081 TCTCAAGGCCCAACACAGTAAACATGATTTGCAATCACACTTCTGCCGATGATG 1140
1141 TCTAAACTGGATGTTTACAGACAAGTTCATTTTATTTAGACGTTTCCCTGCCAGCAACA 1200
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1201 CTACCAAGTGTACGGCAGCAACAGACCTGCCCAACCAATTTACATGTGGAATTAATCAC 1260
1201 CTACCAAGTGTACGGCAGCAACAGACCTGCCCAACCAATTTACATGTGGAATTAATCAC 1260
1261 ATCTCAGATGCTCGCTCAGGAAGATTTATGTTTTCTCGATGCTGAGATGACTCA 1320
1261 ATCTCAGATGCTCGCTCAGGAAGATTTATGTTTTCTCGATGCTGAGATGACTCA 1320
1321 ACAGATGGAATTCATCTGTGGAACCAACAGGAGCTGGATGAAGAGACCTGTGAG 1380
1321 ACAGATGGAATTCATCTGTGGAACCAACAGGAGCTGGATGAAGAGACCTGTGAG 1380
1381 TGTGCTGCAGAGCGGGCTTCGGCTGCGAGTGTGACCAACCAACCAACCAACCAACCA 1440
1381 TGTGCTGCAGAGCGGGCTTCGGCTGCGAGTGTGACCAACCAACCAACCAACCAACCA 1440
1441 AACTCATGCGAGTGTGCTGTAAACCAACCTTCCCGAGCAATGTGGGGCAACCGA 1500
1441 AACTCATGCGAGTGTGCTGTAAACCAACCTTCCCGAGCAATGTGGGGCAACCGA 1500
1501 GAATTTGATGAAAAACACATGCCAGTGTGTATGTAAAGAACCTGCCCGCAACCAACCC 1560
1501 GAATTTGATGAAAAACACATGCCAGTGTGTATGTAAAGAACCTGCCCGCAACCAACCC 1560
1561 CTAAATCTGGAAAAATGTGCTGTGAATGTACAGAAAGTCCACAGAAATGCTTTGTTAAA 1620
1561 CTAAATCTGGAAAAATGTGCTGTGAATGTACAGAAAGTCCACAGAAATGCTTTGTTAAA 1620
1621 GGAAGAAAGTCCACCAACCAACATGCACTGTTCAGACGGCATGTACGAACCGCCAG 1680
1621 GGAAGAAAGTCCACCAACCAACATGCACTGTTCAGACGGCATGTACGAACCGCCAG 1680
1681 AAGGCTTGTGAGCCAGGATTTTATATAGTGAAGAGTGTGTGTTGTGCTTCAATAT 1740
1681 AAGGCTTGTGAGCCAGGATTTTATATAGTGAAGAGTGTGTGTTGTGCTTCAATAT 1740
1741 TGGAAAAAGCAACCAATGAGCTTAATCTAGGATCCGTACCGTCCCGAGCTTTTGTCAAAC 1800
1741 TGGAAAAAGCAACCAATGAGCTTAATCTAGGATCCGTACCGTCCCGAGCTTTTGTCAAAC 1800
1801 AGCACCTTTGTGTTCTTCACTTGGTGAAGCTCTCTACCTGTGTGTGGGAGCGCTGGAT 1860
1801 AGCACCTTTGTGTTCTTCACTTGGTGAAGCTCTCTACCTGTGTGTGGGAGCGCTGGAT 1860
1861 TCTTCTACACACCATGTCCCGCGGAGAGTGGAGACCAACAGTAAAGCTTGTCTCT 1920
1861 TCTTCTACACACCATGTCCCGCGGAGAGTGGAGACCAACAGTAAAGCTTGTCTCT 1920
1921 GAATTTCTATCCCAAGTCTTACCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1980
1921 GAATTTCTATCCCAAGTCTTACCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1980

Db 4141 AGAAGAACTCGTCAAGAGGGGATAGAGGGGATCGCGTGCAGATCGGGAGCGGGATAC 4200
QY 4201 CGTAAAGCAGGAGGAGCGGTGAGCCGATTCGCGCCCAAGCTCTTCAGCAATATCACGGG 4260
Db 4201 CGTAAAGCAGGAGGAGCGGTGAGCCGATTCGCGCCCAAGCTCTTCAGCAATATCACGGG 4260
QY 4261 TAGCCAAAGCTATGTCCTGATAGCGGTGCGCCACACCCAGCGCGCCACAGTCAATC 4320
Db 4261 TAGCCAAAGCTATGTCCTGATAGCGGTGCGCCACACCCAGCGCGCCACAGTCAATC 4320
QY 4321 CAGAAAAGCGGCATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTACGA 4380
Db 4321 CAGAAAAGCGGCATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTACGA 4380
QY 4381 CGAGATCTCGCGTCGCGCATGCGCTTCAGCTGCGCAACAGTTCGGTGGCGGA 4440
Db 4381 CGAGATCTCGCGTCGCGCATGCGCTTCAGCTGCGCAACAGTTCGGTGGCGGA 4440
QY 4441 GCGCCTGATGCTCTTCGTCAGATCATCTGATCGCAAGACCGGCTTCATCCGAGTAC 4500
Db 4441 GCGCCTGATGCTCTTCGTCAGATCATCTGATCGCAAGACCGGCTTCATCCGAGTAC 4500
QY 4501 GTGTCGCTCGATGCGATGTTTCGCTTGGTTCGATGCGGAGTGGGATCAAGCG 4560
Db 4501 GTGTCGCTCGATGCGATGTTTCGCTTGGTTCGATGCGGAGTGGGATCAAGCG 4560
QY 4561 TATGAGCGCGCGCATGTCATGAGCATGATGATGATGATGATGATGATGATGATGATG 4620
Db 4561 TATGAGCGCGCGCATGTCATGAGCATGATGATGATGATGATGATGATGATGATGATG 4620
QY 4621 ATGACAGGAGATCTCTCCCGGCACTTCGCGGAGTGGGATGATGATGATGATGATGAT 4680
Db 4621 ATGACAGGAGATCTCTCCCGGCACTTCGCGGAGTGGGATGATGATGATGATGATGAT 4680
QY 4681 TGACACGTCGAGCAGCTGCGGAGGAGCGCGTTCGCGGAGTGGGATGATGATGATGATGAT 4740
Db 4681 TGACACGTCGAGCAGCTGCGGAGGAGCGCGTTCGCGGAGTGGGATGATGATGATGATGAT 4740
QY 4741 CTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4800
Db 4741 CTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4800
QY 4801 GGGCGCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4860
Db 4801 GGGCGCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4860
QY 4861 CCCAGTCATAGCGAATAGCTCTCCACCAAGCGCGGAGACCTGCGTGCATCCAT 4920
Db 4861 CCCAGTCATAGCGAATAGCTCTCCACCAAGCGCGGAGACCTGCGTGCATCCAT 4920
QY 4921 CTGTTCAATCATGCGAAGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4980
Db 4921 CTGTTCAATCATGCGAAGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4980
QY 4981 GCGATCAGATCTGTTGGCGGAGAAAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
Db 4981 GCGATCAGATCTGTTGGCGGAGAAAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
QY 5041 TACCAGAGGGCGCCAGCTGCGCAATTCGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5100
Db 5041 TACCAGAGGGCGCCAGCTGCGCAATTCGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5100
QY 5101 CTAGCTATGCGCATGTAAGCCCACTGCAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5160
Db 5101 CTAGCTATGCGCATGTAAGCCCACTGCAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5160
QY 5161 CCCTTGTCCAGATAGCCAGTAGCTGATTCATCCGCGGTCAGACCGCTTCTGCGGAC 5220
Db 5161 CCCTTGTCCAGATAGCCAGTAGCTGATTCATCCGCGGTCAGACCGCTTCTGCGGAC 5220
QY 5221 TGGCTTCTAGTGTTCGCTTCCTTTAGCAGCCCTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 5280

Db 5221 TGGCTTCTAGTGTTCGCTTCCTTTAGCAGCCCTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 5280
QY 5281 GTG 5283
Db 5281 GTG 5283
RESULT 2
AAAL5565
ID AAA15565 standard; DNA; 8349 BP.
XX
AC AAA15565;
XX
DT 28-JUL-2000 (first entry)
XX
DE PMON30464 plasmid.
XX
KW Transgenic plant; insect resistance; cry2Aa delta-endotoxin; Coleopteran; Lepidopteran; Dipteran; plastid transit peptide; zmsu PTP; insecticidal; plasmid targeting peptide; pMON30464 plasmid; expression vector; ds.
KW
XX Synthetic.
OS
XX WO2000026371-A1.
XX
PD 11-MAY-2000.
XX
PF 04-NOV-1999; 99WO-US026086.
XX
PR 04-NOV-1998; 98US-00186002.
XX
PA (MONS) MONSANTO CO.
XX
PI Corbin DR, Romano CP;
XX
DR WPI; 2000-376130/32.
XX
PT New method of expressing insecticidal proteins in plants transformed with a Bacillus thuringiensis delta-endotoxin encoding gene resulting in effective control of susceptible target pests.
PT
XX
PS Example 1; Page 96-99; 104pp; English.
XX
CC Bacillus thuringiensis produce delta-endotoxins during sporulation. These proteins are toxic to certain insects e.g. Lepidopteran and Coleopteran larvae. An insect-resistant transgenic plant has been constructed which contains the delta-endotoxin cry2Ab gene. The present sequence would be used to transfer delta-endotoxin genes into plant cells and for subsequent high expression of the cry2Ab gene. Protection may be attained against insects such as Ostrina spp., Diatraea spp., Helicoverpa spp., and Spodoptera spp., in Zea mays; Heliothis virescens, Helicoverpa spp., Pectinophora spp., in Gossypium hirsutum; Anticarsia spp., Pseudoplusia spp., Epinotia spp., in Glycine max; and Scirpophaga incertulas in Oryza sativa. Expression of the endotoxin by a plant cell produces a fusion protein comprising an amino-terminal plastid transit peptide (zmsu PTP) covalently linked to the delta-endotoxin. The fusion protein functions to localise the delta-endotoxin to a subcellular organelle or compartment

Query Match 42.4%; Score 2240; DB 3; Length 8349;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 2409; Conservative 0; Mismatches 25; Indels 144; Gaps 1;
QY 2706 CTAGACCTAATCAGGTCATAGCTGTTTCCTGTGTGAATGTTATCGGCTCACAATTC 2765
Db 5911 CTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAATGTTATCGGCTCACAATTC 5970
QY 2766 ACACAAATACAGCCGCGAGCAATAAGTGTAAAGCTGGGTGCTTATGAGTACGCTA 2825
Db 5971 ACACAAATACAGCCGCGAGCAATAAGTGTAAAGCTGGGTGCTTATGAGTACGCTA 6030
QY 2826 ACTCACAATTAATGGTGGTTCCTCCTCCTGCTGCGGAAACCTGTCGTGCCA 2885

Db	6031	ACTCACAATTAATTCGCTGGCTCACTGCCCGCTTTCCAGTCGGGAACCTGTCGTGCCA	6090	7025	-----TT	7026
QY	2886	GCTGCATTAATGAATCGGCAACGCGCGGAGAGCGGTGTTGCGTATTTGGGCGCTCTTC	2945	3966	GGGTTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGTC	4025
Db	6091	GCTGCATTAATGAATCGGCAACGCGCGGAGAGCGGTGTTGCGTATTTGGGCGCTCTTC	6150	7027	GGGTTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGTC	7086
QY	2946	CGCTTCTCGCTCACTGACTCGCTGGCTCGGTTCGGTTCGGCTCGGCGAGCGGTATCAGC	3005	4026	CCGGAAGAACGATTCGGAAGCCCCAATTTATAGAGGGCGGCGGTGGAATCGAAATCTCG	4085
Db	6151	CGCTTCTCGCTCACTGACTCGCTGGCTCGGTTCGGTTCGGCTCGGCGAGCGGTATCAGC	6210	7087	CCGGAAGAACGATTCGGAAGCCCCAATTTATAGAGGGCGGCGGTGGAATCGAAATCTCG	7146
QY	3006	TCACCTCAAGAGCGGTAAATACGGTATCCACAGAAATCAGGGGATACGACGGAAGAAAT	3065	4086	TGATGGCAGGTTGGCGTCGTTGGTTCGATTCGAAACCCAGAGTCCCGCTCAGAAG	4145
Db	6211	TCACCTCAAGAGCGGTAAATACGGTATCCACAGAAATCAGGGGATACGACGGAAGAAAT	6270	7147	TGATGGCAGGTTGGCGTCGTTGGTTCGATTCGAAACCCAGAGTCCCGCTCAGAAG	7206
QY	3066	GTGAGCAAAAGCCAGCAAAAGCCAGCAACCGTAAAGGCGCGGTTCGTCGGCGTTTTT	3125	4146	AACTCGTCAAGAGCGGTAGAGCGGATGCGCTCGGAATCGGGAGCGCGGATACCGTAA	4205
Db	6271	GTGAGCAAAAGCCAGCAAAAGCCAGCAACCGTAAAGGCGCGGTTCGTCGGCGTTTTT	6330	7207	AACTCGTCAAGAGCGGTAGAGCGGATGCGCTCGGAATCGGGAGCGCGGATACCGTAA	7266
QY	3126	CCATAGGCTCCGCCCGCTGACGAGCATCAAAATAATCGACGCTCAAGTCAGAGTGCGC	3185	4206	AGCAGAGAAAGCGGTACGCCCATTTCCGCGCCAACTCTTCAGCAATATCAGGGTAGCC	4265
Db	6331	CCATAGGCTCCGCCCGCTGACGAGCATCAAAATAATCGACGCTCAAGTCAGAGTGCGC	6390	7267	AGCAGAGAAAGCGGTACGCCCATTTCCGCGCCAACTCTTCAGCAATATCAGGGTAGCC	7326
QY	3186	AAACCCGACAGGACTATAAAGATACAGGCGTTTTCCCGCTGGAAGCTCCCTCGTGGCTC	3245	4266	AAACGCTATGCTGATAGCGGTCCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAA	4325
Db	6391	AAACCCGACAGGACTATAAAGATACAGGCGTTTTCCCGCTGGAAGCTCCCTCGTGGCTC	6450	7327	AAACGCTATGCTGATAGCGGTCCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAA	7386
QY	3246	TCCTGTTCCGACCCCTGCGGCTTACGGATACCTGTCGCCCTTTCTCCCTCGGGAAGCGT	3305	4326	AAGCGGCCATTTTCCACCATGATATTTGGGAAGCAGGATCGCCATGGGTCAACGACGAGA	4385
Db	6451	TCCTGTTCCGACCCCTGCGGCTTACGGATACCTGTCGCCCTTTCTCCCTCGGGAAGCGT	6510	7387	AAGCGGCCATTTTCCACCATGATATTTGGGAAGCAGGATCGCCATGGGTCAACGACGAGA	7446
QY	3306	GGCGCTTCTCATAGCTACAGCTGAGGTATCTCAGTTCGGTTCAGTTCGTCGCTCAA	3365	4386	TCCTCGCGCTCGCGCATTCGCGCTTCGAGCTTCGCGAACAGTTCGCTTCGCGCGCGCC	4445
Db	6511	GGCGCTTCTCATAGCTACAGCTGAGGTATCTCAGTTCGGTTCAGTTCGTCGCTCAA	6570	7447	TCCTCGCGCTCGCGCATTCGCGCTTCGAGCTTCGCGAACAGTTCGCTTCGCGCGCGCC	7506
QY	3366	GCTGGGCTGTGTGACGAACCCCGCTTACGCCGACCGCTGCGCTTATCCCGTAACTA	3425	4446	TGATGCTTCTGCTCCAGATCATCTGATCGAACAGCGGCTTCATCCCGAGTACGTGCT	4505
Db	6571	GCTGGGCTGTGTGACGAACCCCGCTTACGCCGACCGCTGCGCTTATCCCGTAACTA	6630	7507	TGATGCTTCTGCTCCAGATCATCTGATCGAACAGCGGCTTCATCCCGAGTACGTGCT	7566
QY	3426	TCGCTTTGAGTCCAACCCCGTAAACACGACTTATCGCACTGGCAGCAGCACTGGTAA	3485	4506	CGCTCGATCGATGTTTCGCTTGTGTCGAATGGCAGGTAGCCGATCAAGCGTATGC	4565
Db	6631	TCGCTTTGAGTCCAACCCCGTAAACACGACTTATCGCACTGGCAGCAGCACTGGTAA	6690	7567	CGCTCGATCGATGTTTCGCTTGTGTCGAATGGCAGGTAGCCGATCAAGCGTATGC	7626
QY	3486	CAGGATTAGCAGAGCGAGGTATGAGCGGTGCTACAGAGTTCGTAAGTGGTGGCTAA	3545	4566	AGCGCGCGCATTTGATCAGCCATGATGGATACCTTCGCGCAGCAGCAAGTGAATGAC	4625
Db	6691	CAGGATTAGCAGAGCGAGGTATGAGCGGTGCTACAGAGTTCGTAAGTGGTGGCTAA	6750	7627	AGCGCGCGCATTTGATCAGCCATGATGGATACCTTCGCGCAGCAGCAAGTGAATGAC	7686
QY	3546	CTACGGCTACACTAGAGAACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGTTACCTT	3605	4626	AGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCGCGTTCAGTGACA	4685
Db	6751	CTACGGCTACACTAGAGAACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGTTACCTT	6810	7687	AGGAGATCTTCGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCGCGTTCAGTGACA	7746
QY	3606	CGGAAAAGAGTTGGTAGCTCTTGATCCGCAACAAACACCGCTGGTAGCGGTGGTTT	3665	4686	ACGTCGAGCACAGCTGGCAGGAAGAACGCCGCTCGTGGCCAGCAAGATAGCCCGCTGCC	4745
Db	6811	CGGAAAAGAGTTGGTAGCTCTTGATCCGCAACAAACACCGCTGGTAGCGGTGGTTT	6870	7747	ACGTCGAGCACAGCTGGCAGGAAGAACGCCGCTCGTGGCCAGCAAGATAGCCCGCTGCC	7806
QY	3666	TTTTGTTTCAACGACAGATTAAGCGGCAAAAGAGTCTCAAGAGATCCTTTGAT	3725	4746	TCGCTCTGAGTTCATTTAGGGCACCGGACAGGTCTTGACAAAAGAAACCGGGCGC	4805
Db	6871	TTTTGTTTCAACGACAGATTAAGCGGCAAAAGAGTCTCAAGAGATCCTTTGAT	6930	7807	TCGCTCTGAGTTCATTTAGGGCACCGGACAGGTCTTGACAAAAGAAACCGGGCGC	7866
QY	3726	CTTTTCTACGGGTCTGACGCTCAGTGGAAACAACTACAGTTAAAGGATTTTGGTCAT	3785	4806	CCTTCGCTTGACAGCGGAAACACCGCGGCATCAGAGCAGCCGATTCGTTGTGCCAG	4865
Db	6931	CTTTTCTACGGGTCTGACGCTCAGTGGAAACAACTACAGTTAAAGGATTTTGGTCAT	6990	7867	CCTTCGCTTGACAGCGGAAACACCGCGGCATCAGAGCAGCCGATTCGTTGTGCCAG	7926
QY	3786	GAGATTATCGTCAACAAAGCGGCTATGTCCTCCCACTCTCTGAGTTTCGCGGCATG	3845	4866	TCATAGCCCAATAGCTCTCCACCCAGCGGCGGAGAACCTTCGCTGCAATCCATCTGT	4925
Db	6991	GAGATTATCAAAAGGATCTTCACCTAGATTCCTT-----	7024	7927	TCATAGCCCAATAGCTCTCCACCCAGCGGCGGAGAACCTTCGCTGCAATCCATCTGT	7986
QY	3846	GATGCGCGGATAGCGCTGCTGTTTCTCGATGCGCGGATTTGCACTGCGCGTAGAA	3905	4926	TCAATCATGCGAAACGATCCTCATCTGCTCTTGATCAGATCTTGATCCCTTCGCGCAT	4985
Db	7025	-----	7024	7987	TCAATCATGCGAAACGATCCTCATCTGCTCTTGATCAGATCTTGATCCCTTCGCGCAT	8046
QY	3906	CTCCGCGAGGTGCTCAGCGCTCAGGACGAGCTGAACCACTCGGAGGGATCGAGCCC	3965	4986	CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTATCTTTGACGGCTTCCCAACCTTACCA	5045
				8047	CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTATCTTTGACGGGCTTCCCAACCTTACCA	8106

QY	5046	GAGGGGCCCCAGCTGGCAATTCGGTTCGCTTGGTGTCCATAAAACCGCCAGTCTAGC	5105		
Db	8107	GAGGGGCCCCAGCTGGCAATTCGGTTCGCTTGGTGTCCATAAAACCGCCAGTCTAGC	8166		
QY	5106	TATCGGCATGTAAAGCCACCTGAAGCTACCTGCTTCTCTTTGCGCTTGCGTTTCCGCTT	5165		
Db	8167	TATCGGCATGTAAAGCCACCTGAAGCTACCTGCTTCTCTTTGCGCTTGCGTTTCCGCTT	8226		
QY	5166	GTCAGATAGCCCCAGTAGCTGACATTCATCCGGGTGAGCACCGCTTCTCGGACCTGGCT	5225		
Db	8227	GTCAGATAGCCCCAGTAGCTGACATTCATCCGGGTGAGCACCGCTTCTCGGACCTGGCT	8286		
QY	5226	TTCTACGTGTTCCGCTTCCCTTTAGCAGCCCTTGCGCCCTGAGTCCTTGGCGACGCGT	5283		
Db	8287	TTCTACGTGTTCCGCTTCCCTTTAGCAGCCCTTGCGCCCTGAGTCCTTGGCGACGCGT	8344		
RESULT 3					
AAV29673/C					
ID	AAV29673 standard; cDNA; 6136 BP.				
XX	AC	AAV29673;			
XX	AC				
DT	01-SEP-1998 (first entry)				
XX	Hybrid NAMK.6 (termamyl-linker-CBDEGV) nucleotide sequence.				
DE					
XX	Starch; liquefaction; sweetener; enzyme hybrid; endoglucanase; enzyme;				
KW	cellulose binding domain; CBD; starch processing; alpha-amylase;				
KW	saccharification; Termamyl-linker-CBD fusion; ss.				
XX					
OS	Bacillus sp.				
OS	Humicola insolens.				
XX					
PN	WO9816633-A1.				
XX					
PD	23-APR-1998.				
XX					
PF	13-OCT-1997; 97WO-DK000448.				
XX					
PR	11-OCT-1996; 96DK-00001130.				
XX					
PA	(NOVO) NOVO-NORDISK AS.				
XX					
PI	Bjornvad M, Pedersen S, Schulein M, Bisgardfrantzen H;				
XX					
DR	WPI; 1998-251283/22.				
XX					
PT	Liquefaction of starch for, e.g. production of sweeteners - comprises use				
PT	of enzyme hybrids including cellulose binding domain for starch.				
XX					
PS	Example 8; Page 65-67; 83pp; English.				
XX					
CC	This is the nucleotide sequence of the termamyl-linker-CBDEGV fusion				
CC	construct pNAMK6.1. This is an enzyme hybrid which can be used for the				
CC	liquefaction of starch. The enzyme hybrids contain amino acid sequences				
CC	of alpha-amylase linked to a cellulose binding domain (CBD). The CBD is				
CC	selected from the Bacillus or Humicola insolens endoglucanase, C. xylanase A				
CC	or the Humicola insolens EGV sequence. The starch is liquefied by				
CC	treating, in aqueous medium, with such an enzyme hybrid. A recombinant				
CC	expression vector comprising a construct containing isolated DNA encoding				
CC	enzyme hybrids with amylolytic activity, promoter and stop signals can be				
CC	used to transform host cells for the production of the recombinant enzyme				
CC	hybrids. The enzyme hybrids are useful in industrial starch processing				
CC	especially for the production of sweeteners. Hybrid enzymes have altered				
CC	affinity for substrate and increased activity, resulting in at least 1 of				
CC	reduced calcium ion dependence, reduced formation of Maillard reaction				
CC	products and reduced effect of alpha-amylase on subsequent				
CC	saccharification				
XX					
SO	Sequence 6136 BP; 1475 A; 1545 C; 1712 G; 1404 T; 0 U; 0 Other;				

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XX	Sequence	4800 BP; 1345 A; 1032 C; 1163 G; 1260 T; 0 U; 0 Other;	Db	4016	GATGCGAGTTGGCGTCGCTTGGTTCGCTCAATTCGAAACCCCAAGTCCCGCTCAGAAAG	3957
SQ	Query Match	33.9%; Score 1793.4; DB 2; Length 4800;	QY	4147	ACTCGTCAAGAGCGGATAGAGCGATGCGCTCGAATCGGAGCGCGGATACCGTAAA	4206
	Best Local Similarity	91.8%; Pred. No. 3.1e-263;	Db	3956	ACTCGTCAAGAGCGGATAGAGCGGATGCGCTCGAATCGGAGCGCGGATACCGTAAA	3897
	Matches 1980; Conservative	0; Mismatches 1; Indels 176; Gaps 1;	QY	4207	GCACGAGAAAGCGGTACGCCCATTCGCCGCCAAGCTCTTCAGCAATATACCGGTAGCCA	4266
QY	3127	CATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGTGGCGA	Db	3896	GCAAGAGAAAGCGGTACGCCCATTCGCCGCCAAGCTCTTCAGCAATATACCGGTAGCCA	3837
Db	4800	CATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGTGGCGA	QY	4267	ACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCGCGGCACAGTCGATGATCCAGAAA	4326
QY	3187	AACCCGACAGGACTATAAGATACAGAGGTTTCCCGCTGAGAGTCCCTCGTGGCTCT	Db	3836	ACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCGCGGCACAGTCGATGATCCAGAAA	3777
Db	4740	AACCCGACAGGACTATAAGATACAGAGGTTTCCCGCTGAGAGTCCCTCGTGGCTCT	QY	4327	ACGCGCCATTTTCCACCATGATATTCGCAAGCAGGCTATCGCATCGGTGAGTACGAGAT	4386
QY	3247	CCTGTTCCGACCCCTGACCGGATACCGGATACCGCTTCTCCCTTCGGGAAAGCGTG	Db	3776	ACGCGCCATTTTCCACCATGATATTCGCAAGCAGGCTATCGCATCGGTGAGTACGAGAT	3717
Db	4680	CCTGTTCCGACCCCTGACCGGATACCGGATACCGCTTCTCCCTTCGGGAAAGCGTG	QY	4387	CCTCGCCGTCCGGCATGCGGCTTTGAGCTCGCGCAAGTTCGGTGGCGGAGGCCCT	4446
QY	3307	GGGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTGTAGTCCCTCGTCCAAAG	Db	3716	CCTCGCCGTCCGGCATGCGGCTTTGAGCTCGCGCAAGTTCGGTGGCGGAGGCCCT	3657
Db	4620	GGGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTGTAGTCCCTCGTCCAAAG	QY	4447	GATGCTCTTCGTCAGATCATCTGATCGAAGACCGGCTTCCATCCGAGTACGTGCTC	4506
QY	3367	CTGGGCTGTGTGAAGAACCCCGCTTACGCCGACCGCTGCGCTTATCCGCTAACTAT	Db	3656	GATGCTCTTCGTCAGATCATCTGATCGAAGACCGGCTTCCATCCGAGTACGTGCTC	3597
Db	4560	CTGGGCTGTGTGAAGAACCCCGCTTACGCCGACCGCTGCGCTTATCCGCTAACTAT	QY	4507	GCTCGATGCGATGTTTCGCTTGGTTCGATCGAATGGGCGAGTCCGATCAAGCGTATGCA	4566
QY	3427	CGCTTTGAGTCCAAACCGGTAAACACGACTTATCGCCACTGGCAGCAGCACTGTAAC	Db	3596	GCTCGATGCGATGTTTCGCTTGGTTCGATCGAATGGGCGAGTCCGATCAAGCGTATGCA	3537
Db	4500	CGCTTTGAGTCCAAACCGGTAAACACGACTTATCGCCACTGGCAGCAGCACTGTAAC	QY	4567	GCGCGCGCATGTCATCAGCCATGATGATATCTTCGCGGAGGAGCAAGGTGAGATGACA	4626
QY	3487	AGGATTAGCAGACGAGGATGTAGGCGGTGTACAGAGTTCCTGAAGTGTGGGCTTAAC	Db	3536	GCGCGCGCATGTCATCAGCCATGATGATATCTTCGCGGAGGAGCAAGGTGAGATGACA	3477
Db	4440	AGGATTAGCAGACGAGGATGTAGGCGGTGTACAGAGTTCCTGAAGTGTGGGCTTAAC	QY	4627	GGAGATCTCTCCCGGCACTTCGCCAATAGCAGCCAGTCCCTTCCCGTTCAGTGACAA	4686
QY	3547	TACGGCTACACTAGAGAACAGTATTGGTATCTGGCTCTGCTGAAGCCAGTTACTTTC	Db	3476	GGAGATCTCTCCCGGCACTTCGCCAATAGCAGCCAGTCCCTTCCCGTTCAGTGACAA	3417
Db	4380	TACGGCTACACTAGAGAACAGTATTGGTATCTGGCTCTGCTGAAGCCAGTTACTTTC	QY	4687	CGTCGAGCAGCTGCGCAAGAAACCGCTCGTGGCCAGCCACGATAGCCGCGTGCCT	4746
QY	3607	GGAAAGAGTTCGTAGCTCTTGATCCGGCAAAACCAACCGCTGTAGCGGTGGTTTT	Db	3416	CGTCGAGCAGCTGCGCAAGAAACCGCTCGTGGCCAGCCACGATAGCCGCGTGCCT	3357
Db	4320	GGAAAGAGTTCGTAGCTCTTGATCCGGCAAAACCAACCGCTGTAGCGGTGGTTTT	QY	4747	CGTCTCTGCAATTCATTCAGGGCACCGGACAGGTTCGTTGACAAAAGAACCGGGGCC	4806
QY	3667	TTTGTGTTGCAAGCAGCAGATTAACCGCGAGAAAAAAGGATCTCAAGAGATCTTTGATC	Db	3356	CGTCTCTGCAATTCATTCAGGGCACCGGACAGGTTCGTTGACAAAAGAACCGGGGCC	3297
Db	4260	TTTGTGTTGCAAGCAGCAGATTAACCGCGAGAAAAAAGGATCTCAAGAGATCTTTGATC	QY	4807	CCTGCGCTGACAGCGGAAACACCGCGCATCAGAGCCGATTTGCTGTTGTCGCCAGT	4866
QY	3727	TTTCTACGGGCTGACGCTCAGTGAAACGAAACTCAGTTAAGGATTTTGGTCAATG	Db	3296	CCTGCGCTGACAGCGGAAACACCGCGCATCAGAGCCGATTTGCTGTTGTCGCCAGT	3237
Db	4200	TTTCTACGGGCTGACGCTCAGTGAAACGAAACTCAGTTAAGGATTTTGGTCAATG	QY	4867	CATAGCCGAATAGCTCTCCACCCAGCGCCGAGAACCTGCGTGCATTCATTCATCTGTT	4926
QY	3787	AGATTATCGTCGACAAAGCGGCATCGTGCCTCCCACTCCCTGCAAGTTCGGGGGCATG	Db	3236	CATAGCCGAATAGCTCTCCACCCAGCGCCGAGAACCTGCGTGCATTCATTCATCTGTT	3177
Db	4141	-----	QY	4927	CAATCATCGGAAACGATCTCATCTCTTCATCAGATCTTCATTCATTCATTCATTCAT	4986
QY	3847	ATGCGCGGATAGCGGTCTGGTTTCTTGATGCGGACCGGATTTGCACTGCCGTAGAAC	Db	3176	CAATCATCGGAAACGATCTCATCTCTTCATCAGATCTTCATTCATTCATTCATTCAT	3117
Db	4141	-----	QY	4987	AGATCTTGGCGGCAAGAAAGCCATCAGTTTACTTTGCGGGCTTCCCAACCTTACCAAG	5046
QY	3907	TCCCGAGGTCGTCCAGCTCAGCAGCAGCTGAACCACTCGCGAGGGATCGAGCCG	Db	3116	AGATCTTGGCGGCAAGAAAGCCATCAGTTTACTTTGCGGGCTTCCCAACCTTACCAAG	3057
Db	4141	-----	QY	5047	AGGCGCCCAAGCTGGCAATTCGCGTTTCGCTTGTCTCCATTAACCCGCGCAGTCTAGCT	5106
QY	3967	GGGTGGGGAAGAACTCCAGCATAGATCCCGGCTGGAGGATCATCCAGCCGGGTCC	Db	3056	AGGCGCCCAAGCTGGCAATTCGCGTTTCGCTTGTCTCCATTAACCCGCGCAGTCTAGCT	2997
Db	4136	GGGTGGGGAAGAACTCCAGCATAGATCCCGGCTGGAGGATCATCCAGCCGGGTCC	QY	5107	ATCGCCATGTAAAGCCCACTGCAAGCTACTCTCTTCTTTGCGCTTCGCTTTTCCCTTG	5166
QY	4027	CGGAAACAGTATCCGAAACCCAACTTTTCATAGAGGCGGCGGTGGAATCGAATCTCGT	Db	2996	ATCGCCATGTAAAGCCCACTGCAAGCTACTCTCTTCTTTGCGCTTCGCTTTTCCCTTG	2937
Db	4076	CGGAAACAGTATCCGAAACCCAACTTTTCATAGAGGCGGCGGTGGAATCGAATCTCGT	QY	5167	TCCAGATAGCCAGTGTAGCTGACATTCATCCGCGGTTCAGACCGTTCCTGCGACCTGGCT	5226
QY	4087	GATGGCAGGTTGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	Db	2936	TCCAGATAGCCAGTGTAGCTGACATTCATCCGCGGTTCAGACCGTTCCTGCGACCTGGCT	2877

QY 5227 TCTAGTGTTCGGCTTCCTTTAGAGCCCTTGGCGCCCTGAGTGTCTGGCGAGCGTG 5283
 Db 2876 TCTACGTGTTCGGCTTCCTTTAGCAGCCCTTGGCGCCCTGAGTGTCTGGCGAGCGTG 2820

RESULT 5
 AAV33629/c
 ID AAV33629 standard; DNA; 5594 BP.
 AC AAV33629;
 XX
 XX 29-DEC-1998 (first entry)
 XX
 XX
 DE GENSA 981, a monomeric DNA sequence produced by the invention.
 XX
 KW Class IIS restriction endonuclease recognition site;
 KW endogenous mouse promoter element; tissue-specific gene expression;
 KW hormone-specific gene expression; ss;
 KW developmental-specific gene expression.
 XX
 OS Synthetic.
 XX
 XX WO9838326-A1.
 XX
 XX 03-SEP-1998.
 XX
 XX 28-FEB-1998; 98WO-US003918.
 XX
 XX 28-FEB-1997; 97US-0070910P.
 PR
 XX (NATU-) NATURE TECHNOLOGY CORP.
 PA
 XX Hodgson CP, Zink MA, Xu G;
 PI
 XX WPI; 1998-495399/42.
 DR
 XX
 XX Method for assembling gene or gene vector - comprises use of primers
 PT containing class IIS restriction endonuclease recognition sites.
 PT
 XX Example 2; Page 107-110; 141pp; English.
 PS
 XX The invention provides a novel method for directing self-assembly of a
 CC gene having three or more fragments in a directionally and spatially
 CC ordered fashion to produce a gene or a gene vector. The method involves
 CC usage of primers, containing class IIS restriction endonuclease
 CC recognition sites, for isolation of these fragments. As described in the
 CC disclosure, the method may also use a vector for the incorporation and
 CC screening of endogenous mouse promoter elements for the identification of
 CC cell specific promoters. In the example given, plasmids pBK-CMV
 CC (AAV33626), pVLMB (AAV33623) and pVLONGH-900 (AAV33621) were used as
 CC templates from which six fragments were amplified. Each of the fragments
 CC contained different regulatory sequences. The six PCR fragments were
 CC designed to self-assemble into a retro-vector using the method of the
 CC invention. The present sequence, designated as GENSA 981, represents the
 CC monomeric DNA sequence of the six ligated fragments. In general, the
 CC method is claimed to be useful for isolating and identifying regulatory
 CC sequences from a cell, including those for enhanced biological activity,
 CC or tissue-specific, hormone-specific or developmental-specific gene
 CC expression
 XX
 SQ Sequence 5594 BP; 1232 A; 1519 C; 1518 G; 1325 T; 0 U; 0 Other;

Query Match 31.3%; Score 1652.4; DB 2; Length 5594;
 Best Local Similarity 85.4%; Pred. No. 7.3e-242;
 Matches 1916; Conservative 0; Mismatches 261; Indels 67; Gaps 4;

QY 3107 CGCGTGTCTGGCGTTTTCCTAGGTCTCCGCCCTTGGCGCCCTGAGTGTCTGGCGAGCGTG 3166
 Db 5591 CGCGGTGTCTGGCGTTTTCCTAGGTCTCCGCCCTTGGCGCCCTGAGTGTCTGGCGAGCGTG 5532

QY 3167 GCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATTAAGTACACGCGGTTTCCCGCTG 3226
 Db

Db 5531 GCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATTAAGATACACGAGGCTTTCCCGCTG 5472
 QY 3227 GAAGTCCCTCGTGGCTCTCTGTTCGACCTCGCGCTTACCGGATACCTGTCCGCTG 3286
 Db 5471 GAAGTCCCTCGTGGCTCTCTGTTCGACCTCGCGCTTACCGGATACCTGTCCGCTG 5412
 QY 3287 TTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTACGCTGAGTATCTCACTTCGG 3346
 Db 5411 TTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTACGCTGAGGTATCTCACTTCGG 5352
 QY 3347 TGTAGTTCGTTTCGCTCCAAGCTGGGCTGTGTGCAGAACCCCGCTTACGCGGACCGCT 3406
 Db 5351 TGTAGTTCGTTTCGCTCCAAGCTGGGCTGTGTGCAGAACCCCGCTTACGCGGACCGCT 5292
 QY 3407 GCGCTTTATCCGTTAACTATCTGTGAGTCAACCCGTTAAGACACGACTTATCGCAC 3466
 Db 5291 GCGCTTTATCCGTTAACTATCTGTGAGTCAACCCGTTAAGACACGACTTATCGCAC 5232
 QY 3467 TGGCAGCAGCCACTGTGTAACAGGATTAGCAGAGGAGTATGTAGGCGGTCTACAGAGT 3526
 Db 5231 TGGCAGCAGCCACTGTGTAACAGGATTAGCAGAGGAGTATGTAGGCGGTCTACAGAGT 5172
 QY 3527 TCTTGAAGTGGTGGCTTAACTAGCGCTACACTAGAAGAACAGTATTTGGTATCTCGGCTC 3586
 Db 5171 TCTTGAAGTGGTGGCTTAACTAGCGCTACACTAGAAGAACAGTATTTGGTATCTCGGCTC 5112
 QY 3587 TGTGAAGCCAGTTACCTTCGGAAGAGTGTGGTAGCTCTTGATCCGGAACAAACCA 3646
 Db 5111 TGTGAAGCCAGTTACCTTCGGAAGAGTGTGGTAGCTCTTGATCCGGAACAAACCA 5052
 QY 3647 CCGCTGTAGCGGTGGTGTGTTTGTGCAAGCAGCAGATTACGCGCAGAAACCAAGAT 3706
 Db 5051 CCGCTGTAGCGGTGGTGTGTTTGTGCAAGCAGCAGATTACGCGCAGAAACCAAGAT 4992
 QY 3707 CTCAGAAGATCTTTGATCTTTCTACGGGTCTGACGCTC-----AGTGAACG 3757
 Db 4991 GGTGTGGGCTCTTTATTGAGCTCGGGAGCAGAACGCGCGCAACAGAGCGAAGCG 4932
 QY 3758 AAAACTCAGTTAAGGATTTTGGTCAAGATTTGCTGATGATTTGCTGCAAAAGCGGCAATCGTGC 3817
 Db 4931 AACTGATGTTAGTTCAAAATAAGGCACAGGGTCAITTTAGGTCCTTGGGGCACCTTGA 4872
 QY 3818 CTC-----CCCACTCTCTGAGTTCCGGGGCATGATGCGCGATAGCCGCTG 3864
 Db 4871 AACATCTGATGTTCTCTAGAAGTCTGAGGCTGACCGCATCTGGGACCATCTGTT 4812
 QY 3865 CTGGTTCTCGATGCGGACGATTTGC-----ACTGCGGTAGAACTCCGCGAG 3914
 Db 4811 CTGGCCCTGAGCGGGGCGAGAACTGCTTACCACAGATATCTGTTTGGCCCATATTCA 4752
 QY 3915 GTGCTCCAGCTCAGCAGCAGTGNACCACTCGCGAGGGGATCGAGCCGGGGTGGG 3974
 Db 4751 GCTGTTCCATCTGTTCTTGGCCCTGAGCGGGGCGAGAACTGCTTACCACAGATATCTG 4692
 QY 3975 GAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGCTCCCGGAAAC 4034
 Db 4691 TTTGGCCCATATTCAGCTGTTCCATCTGTTCTGACCTTGATCTGAACTTCTTATCTC 4632
 QY 4035 GATTCCGAAGCCCAACCTTTTCATGAAGCGCGGTGGAATCGAAATCTCG----- 4085
 Db 4631 AGTTATGATTTTTCATGCTTGCATAAATGCGGTTACTTAAAGTAGCTTGCACAACTA 4572
 QY 4086 -----TGATGGCAGGTTGGGCGTCTGCTTGGTTCGTTCA 4119
 Db 4571 CAGTGGGGTCTTTCATTTCCCGCTTTTCTGGAGGTTGGGCGTCTGCTGCGTCA 4512
 QY 4120 TCGAACCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAGGCGATAGAGGCGATCGCT 4179
 Db 4511 TCGAACCCAGAGTCCCGCTCAGAAAGAACTCGTCAAGAGGCGATAGAGGCGATCGCT 4452
 QY 4180 GCGAATCGGAGCGCGATACCGTAAAGCAGAGGAGCGGTGAGGCGGATTCGCGCCAA 4239
 Db 4451 GCGAATCGGAGCGCGATACCGTAAAGCAGAGGAGCGGTGAGGCGGATTCGCGCCAA 4392


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QY 3602 CCTTCGGAAGAAGTTGGTAGCTCTTGATCCGGGAACAAACCAACCGCTGGTAGCGGTG 3661
Db 4625 CCTTCGGAAGAAGTTGGTAGCTCTTGATCCGGGAACAAACCAACCGCTGGTAGCGGTG 4566
QY 3662 GTTTTGTGTTGCAAGCAGCAGATATAGCGCAGAGAAAAGGATCTCAAGAAATCCTT 3721
Db 4565 GTTTTGTGTTGCAAGCAGCAGATATAGCGCAGAGAAAAGGATCTCAAGAAATCCTT 4506
QY 3722 TGATCTTTTCTACGGGCTCTGACGCTCAGTGAAGCAAGAACTCACTGAAGGATTTTGG 3781
Db 4505 TGATCTTTTCTACGGGCTCTGACGCTCAGTGAAGCAAGAACTCACTGAAGGATTTTGG 4446
QY 3782 TCATGAGATTAATC----- 3794
Db 4445 TCATGAGATTAATCAAAAAGGATCTTCACTAGATCCTTTTAAATTAATAATGAAGTTTAA 4386
QY 3795 -----GTCGACCA 3802
Db 4385 GCACGTGTCAGTCTGTCTCTCGGCCACGAGTGCACGAGTTGCCGGCCGGGTCGGCGCA 4326
QY 3803 AAGCGCCATCGTGCCTCCCACTCTCTGAGTTTCGGGGGCATGATCGCGGATAGCCGC 3862
Db 4325 GGGCGAACTCCGCCCCCAGCGGTGCTCGCGATCTCGGTCAATGCGCGCCCGAGCGGT 4266
QY 3863 TGCTGTGTTTCTGATGCGCAGGATTTGACTCCCGGTAGAACTCCGCGAGGTCGTCCA 3922
Db 4265 CCGGAAAGTTCTGGGACACGACACCTCCGACACTCGCGGTACAGCTCGTCAGGCGCGGCA 4206
QY 3923 GCC----- 3925
Db 4205 CCCACACCCAGGCCAGGTTGTTGCCGACACCTGCTGCTGGAACGCGCTGATGAACA 4146
QY 3926 ----TCAGGCGAGCTGAACAACTCGAGGGGATCGAGCCCGGGTGGCGAAGAACT 3982
Db 4145 GGGTCACGTGCTCCCGGACCAACCGCGGAAGTCTCTCCACGAATCCCGGGAGAAC 4086
QY 3983 CCAGCATGAGATCCCGCGCTGAGGATCATCCAGCGCGGTCCGGAAACGATTCGGA 4042
Db 4085 CGAGCCGGTCCGTCAGAACTCAGACCGCTCCGCGACGTCGCGCGGTGAGCACCGGA 4026
QY 4043 AGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGTGTAGTGGCAGGTTGGCG 4102
Db 4025 CGGCATGTTCACTTGGCCATGGTGGCCCTCTCAGTGTCTAATTGAAGCATTTATC 3966
QY 4103 TCGCTTGGTGGTCAATTTGAAACCCAGAGTCCCG----- 4137
Db 3965 AGGGTTATTGCTCTCATGAGCGGATACATATTTGAAATGATTAGAAAAATAACAAATAG 3906
QY 4138 ----- 4137
Db 3905 GGGTTCGCGCACATTTCCCGAAAAAGTGCCACCTGTATGCGGTGTGAATAACCGCACAG 3846
QY 4138 -----CTCAGAAGAACTC 4150
Db 3845 ATGCGTAAGAGAAAAATACGCATCAGAAATTTGAAGCGTTAATAATTCAGAAGAACTC 3786
QY 4151 GTCAAGAAGCGGATAGAAGCGATGCGTCCGAATCCGGAGCGCGATACCGTAAAGCAC 4210
Db 3785 GTCAAGAAGCGGATAGAAGCGATGCGTCCGAATCCGGAGCGCGATACCGTAAAGCAC 3726
QY 4211 GAGGAAGCGGTGAGCCCATTCGCGCCCAAGCTTTTCAGCAATATACGGGTAGCCAAACG 4270
Db 3725 GAGGAAGCGGTGAGCCCATTCGCGCCCAAGCTTTTCAGCAATATACGGGTAGCCAAACG 3666
QY 4271 TATGTCCTGATAGCGGTCCGCGCACACCCAGCGCGGCACAGTCGATCAATCCGAAAGCG 4330
Db 3665 TATGTCCTGATAGCGGTCCGCGCACACCCAGCGCGGCACAGTCGATCAATCCGAAAGCG 3606
QY 4331 GCATTTTCCACATGATATTCGCAAGCAGGCGCATCGCATGGGTACAGCAGAGATCCTC 4390
Db 3605 GCCATTTTCCACATGATATTCGCAAGCAGGCGCATCGCATGGGTACAGCAGATCCTC 3546
QY 4391 GCCGTGGGCGATCGCGGCTTTGAGCCTTGCGGAACAGTTTCGGTGGCGCGAGCCCTTGATG 4450
```

RESULT 8

AAV33630/c

ID AAV33630 standard; DNA; 6561 BP.

XX AAV33630;

AC AAV33630;

XX 29-DEC-1998 (first entry)

XX Plasmid VLSNO2

DNA sequence used in the method of the invention.

XX Class IIS restriction endonuclease recognition site; IIR;

XX endogenous mouse promoter element; tissue-specific gene expression;

XX hormone-specific gene expression; mouse VL30 genome;

OS Synthetic.
 PN WO200261037-A2.
 XX 08-AUG-2002.
 PD 12-DEC-2001; 2001WO-US048726.
 XX 12-DEC-2000; 2000US-0255021P.
 PR (BAYU) BAYLOR COLLEGE MEDICINE.
 XX (ADVI-) ADVISYS.
 PA Schwartz RJ, Carpenter RH, Draghia-Akli R, Kern DR, Smith RG;
 PI WPI; 2002-619237/66.
 DR Improving or enhancing growth, lean body mass, milk production, feed
 PT efficiency or Insulin-like Growth Factor-I levels, comprises introducing
 PT a vector encoding a growth hormone releasing hormone into an animal
 PT before or during gestation.
 XX
 PS Example 2; Page 109-111; 113pp; English.
 XX
 CC The present sequence represents vector pSPc5-12-HV-GHRH, which carries
 CC cDNA encoding pig growth hormone releasing hormone (GHRH) cDNA. Nucleic
 CC acids encoding GHRH are used in the method of the invention. The
 CC specification describes a method for improving or enhancing
 CC characteristics e.g. growth, lean body mass, Insulin-like Growth Factor
 CC (IGF)-I levels, growth rate and milk production in an offspring, and for
 CC delaying birth of an offspring. The method comprises introducing a
 CC vector, encoding GHRH, into cells of the female animal prior to or during
 CC gestation of the offspring under conditions where the nucleotide sequence
 CC is expressed. The method is useful of improving or enhancing animal
 CC growth, for increasing growth hormone, lean body mass, IGF-I levels, feed
 CC efficiency, growth rate, ratio of somatotrophs to other hormone-producing
 CC cells in a pituitary gland, and milk production in an offspring, and for
 CC delaying birth of an offspring. GHRH nucleic acids and vectors are used
 CC for diagnostic purposes in clinical medicine, both human and veterinary.
 CC e.g. in treating growth-related disorders such as hypopituitary dwarfism
 CC resulting from abnormalities in growth hormone production, and in
 CC stimulating the growth and enhancing feed conversion efficiency of
 CC animals raised for meat, milk and egg production
 XX
 SQ Sequence 3534 BP; 764 A; 1018 C; 979 G; 773 T; 0 U; 0 Other;
 Query Match 30.4%; Score 1603.8; DB 6; Length 3534;
 Best Local Similarity 82.8%; Pred. No. 1.8e-234;
 Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;
 QY 2706 CTAGACGTAATCATGTCATAGCTGTTTCTGTGTGAATTTGTAATTCGCTCACAAATCC 2765
 DB 1412 CTTGGCGTAATCATGTCATAGCTGTTTCTGTGTGAATTTGTAATTCGCTCACAAATCC 1471
 QY 2766 ACACAAACATACGAGCGGGAAGCATAAAGTGAAGCTGGGTGCTTAATGATGAGCTA 2825
 DB 1472 ACACAAACATACGAGCGGGAAGCATAAAGTGAAGCTGGGTGCTTAATGATGAGCTA 1531
 QY 2826 ACTCAATTAATTTGGTTCGCTCACTGCGCGGTTCACAGTCCGGAACCTCTCGTGCCA 2885
 DB 1532 ACTCAATTAATTTGGTTCGCTCACTGCGCGGTTCACAGTCCGGAACCTCTCGTGCCA 1591
 QY 2886 GGTGCATTAATGAATCGGCCAACGCGCGGGGAGAGCGGTTTTCGTAATTTGGCGCTCTTC 2945
 DB 1592 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGCGGTTTTCGTAATTTGGCGCTCTTC 1651
 QY 2946 CGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3005
 DB 1652 CGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 1711
 QY 3006 TCACTCAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATACGCGAGGAAGCAAT 3065
 DB 1712 TCACTCAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATACGCGAGGAAGCAAT 1771

QY 3066 GTGACAAAGGCGCAGCAAAAGGCCAGCAACGCTAAAAAGGCCGCTTGCTGGCGTTTTT 3125
 DB 1772 GTGACAAAGGCGCAGCAAAAGGCCAGCAACGCTAAAAAGGCCGCTTGCTGGCGTTTTT 1831
 QY 3126 CCATAGGCTCGCGCCCTCTGACGAGCATCAAAAATCGAGCTCAAGTCAAGTCAAGTCAAGT 3185
 DB 1832 CCATAGGCTCGCGCCCTCTGACGAGCATCAAAAATCGAGCTCAAGTCAAGTCAAGT 1891
 QY 3186 AAAACCGACAGGACTATAAAGATACAGGCGGTTTTCCCTCGAAAGCTCCCTCGTCGCTC 3245
 DB 1892 AAAACCGACAGGACTATAAAGATACAGGCGGTTTTCCCTCGAAAGCTCCCTCGTCGCTC 1951
 QY 3246 TCCGTTCGAGCCCTCGCGCTTACGGATACCTGTCGCGCTTTCTCCCTCGGAAGCGT 3305
 DB 1952 TCCGTTCGAGCCCTCGCGCTTACGGATACCTGTCGCGCTTTCTCCCTCGGAAGCGT 2011
 QY 3306 GCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGCTGTAGTTCGTTCCCTCAA 3365
 DB 2012 GCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGCTGTAGTTCGTTCCCTCAA 2071
 QY 3366 GCTGGGCTGTGCAAGAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGTAACCTA 3425
 DB 2072 GCTGGGCTGTGCAAGAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGTAACCTA 2131
 QY 3426 TCGTCTTTAGTCCAAACCGGTAGACACGACTTATGCGCACTGGCAGCAGCAGCTGTAA 3485
 DB 2132 TCGTCTTTAGTCCAAACCGGTAGACACGACTTATGCGCACTGGCAGCAGCAGCTGTAA 2191
 QY 3486 CAGGATTAGCAGAGCGAGGTATGAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTTAA 3545
 DB 2192 CAGGATTAGCAGAGCGAGGTATGAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTTAA 2251
 QY 3546 CTAGCGTCACTAGAGAACAGTATTTGATCTGCGCTCTGCTGAAGCCAGTTACTCTT 3605
 DB 2252 CTAGCGTCACTAGAGAACAGTATTTGATCTGCGCTCTGCTGAAGCCAGTTACTCTT 2311
 QY 3606 CGGAAAAAGAGTTGGTAGCTCTTGTATCCGCAAAACAAACCCGCTGGTAGCGGTGTTT 3665
 DB 2312 CGGAAAAAGAGTTGGTAGCTCTTGTATCCGCAAAACAAACCCGCTGGTAGCGGTGTTT 2371
 QY 3666 TTTTGTTCGCAAGCAGCAGATTACGCGCAGAAAAAGAGATCTCAAGAGATCCTTTGAT 3725
 DB 2372 TTTTGTTCGCAAGCAGCAGATTACGCGCAGAAAAAGAGATCTCAAGAGATCCTTTGAT 2431
 QY 3726 CTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCA 3785
 DB 2432 CTTTCTACGGGTCTGTA----- 2449
 QY 3786 GAGATTATCGTCGACCAAGCGGCATCGTGCTCCCACTCTGCGATTGCGGGGCATG 3845
 DB 2450 ----- 2449
 QY 3846 GATGCGGATAGCGCTGCTGTTTCTCGATGCGAGGATTTGCACTGCGCGTAGAA 3905
 DB 2450 ----- 2449
 QY 3906 CTTCCGAGGTGCTCCAGCTCAGGACGAGCTGAAACCACTCGCAGGGGATCGAGCCC 3965
 DB 2450 ----- 2449
 QY 3966 GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGT 4025
 DB 2450 ----- 2449
 QY 4026 CCGAAAAACGATTCGAAAGCCAACTTTTCATAGAAGCGCGGTGGATCGAAATCTCG 4085
 DB 2450 ----- 2449
 QY 4086 TGATGGCAGGTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4145
 DB 2450 -----CGCTCAGAAG 2459

4146 AACTCGTCAAGAGCGGATAGAGGCGATGCGTTCGGAATCGGAGCGGCGATACCGTAA 4205
4206 AGACAGAGGAGCGGTAGCCCATTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 4265
4266 AACGCTATGCTGATAGCGGTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 4325
4326 AACGCGCATTTTCCACCATGATATTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 4385
4386 TCCCTCGCGGTGCGGATGCGGCTTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 4445
4446 TGATGCTCTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 4505
4506 CGCTCGATGCGATGTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 4565
4566 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 4625
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4806 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 4865
4866 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 4925
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5926 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 5985
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6166 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 6225
6226 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 6285
6286 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 6345
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6406 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 6465
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8806 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 8865
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8986 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 9045
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9706 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 9765
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9886 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 9945
9946 AGCGCGCATTTTCGTCAGATCATCTTCGCGGCAAGCTCTTCAGCAATATACGGGTAGCC 10005

AA62060;
22-SEP-2003 (first entry)
TV-GHRH plasmid DNA.
Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;
sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;
lymphoma; weight loss; lymphopoeisis; appetite stimulant; anorectic;
growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.
Unidentified.
WO2003049700-A2.
19-JUN-2003.
10-DEC-2002; 2002WO-US039509.
11-DEC-2001; 2001US-0339610P.
(ADVI-) ADVISYS INC.
(BAYU) BAYLOR COLLEGE MEDICINE.
Draghia-Akii R, Carpenter RH, Kern DR, Schwartz RJ, King G;
Hahn K, Brenner MK;
WPI; 2003-558968/52.
Treating anemia, immune dysfunction, tumor, increasing total red blood
cell mass, reversing wasting or abnormal weight loss in subject, by
administering nucleic acid construct encoding growth-hormone-releasing-
hormone.
Claim 4; Page 193-195; 212pp; English.
The invention relates to compositions and methods for plasmid-mediated
supplementation. The method is useful for treating anaemia, tumour (such
as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
kidney failure, for preventing the development of metastatic tumour, for
increasing total red blood cell mass, for reversing wasting, abnormal
weight loss or suppression of lymphopoeisis, in a subject, or for
increasing weight gain in a chronically ill subject or, for extending
life expectancy for a chronically ill subject. The present sequence is TV
-growth hormone releasing hormone (GHRH) plasmid DNA. This sequence is
used to illustrate the method of the invention
Sequence 3534 BP; 764 A; 1016 C; 979 G; 775 T; 0 U; 0 Other;
Query Match 30.4%; Score 1603.8; DB 8; length 3534;
Best Local Similarity 82.8%; Pred. No. 1.8e-234;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;
QY 2706 CTAGAGCGTAATCATAGTTCATAGCTGTTTCTGTTGTAATTTGTTATCCGCTCACAATTC 2765
DB 1412 CTTGGCGTAATCATAGTTCATAGCTGTTTCTGTTGTAATTTGTTATCCGCTCACAATTC 1471
QY 2766 ACACACATACGAGCGGAGAGCATAAAGTCTAAAGCTCGGCTGCTTAATGAGTGAGCTA 2825
DB 1472 ACACACATACGAGCGGAGAGCATAAAGTCTAAAGCTCGGCTGCTTAATGAGTGAGCTA 1531
QY 2826 ACTCACATTAATTTGCGTTCGCTCAGTCCCGCTTTTCAGTTCGGGAAACCTGCTGCCA 2885
DB 1532 ACTCACATTAATTTGCGTTCGCTCAGTCCCGCTTTTCAGTTCGGGAAACCTGCTGCCA 1591
QY 2886 GTTGCATTAATGAGTTCGCGCAACCGCGGAGAGCGGTTTGGTATTTGGCGCTCTTC 2945
DB 1592 GTTGCATTAATGAGTTCGCGCAACCGCGGAGAGCGGTTTGGTATTTGGCGCTCTTC 1651
QY 2946 CGCTTCCTCGCTCAGTTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTATCAGC 3005
DB 1652 CGCTTCCTCGCTCAGTTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTATCAGC 1711

QY 3006 TCACTCAAAGCGGTAATACGGTTATCCACAGAAATCAGGGGATACAGCAGGAGAAACAT 3065
 Db 1712 TCACTCAAAGCGGTAATACGGTTATCCACAGAAATCAGGGGATACAGCAGGAGAAACAT 1771
 QY 3066 GTGAGCAAAAGCCAGCAAAAGCCAGCAACCGTAAAAAGCCGGTTCGCTGGCGTTT 3125
 Db 1772 GTGAGCAAAAGCCAGCAAAAGCCAGCAACCGTAAAAAGCCGGTTCGCTGGCGTTT 1831
 QY 3126 CCATAGGCTCGCCCTCCCTGACAGCATCACAAAAATCGACGCTCAAGTCAGAGTGGCG 3185
 Db 1832 CCATAGGCTCGCCCTCCCTGACAGCATCACAAAAATCGACGCTCAAGTCAGAGTGGCG 1891
 QY 3186 AAAACCGACAGACTATAAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGGCTC 3245
 Db 1892 AAAACCGACAGACTATAAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTGGCTC 1951
 QY 3246 TCCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGGT 3305
 Db 1952 TCCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGGT 2011
 QY 3306 GGCGCTTCTCATAGCTACAGCTGATAGTATCTCAGTTGCGTGTAGGTTCGTTCCGCTCAA 3365
 Db 2012 GGCGCTTCTCATAGCTACAGCTGATAGTATCTCAGTTGCGTGTAGGTTCGTTCCGCTCAA 2071
 QY 3366 GCTGGGCTGTGTCAAGAACCCCGCTTACCGCCGACCGCTGCGCTTATCCCGTAACATA 3425
 Db 2072 GCTGGGCTGTGTCAAGAACCCCGCTTACCGCCGACCGCTGCGCTTATCCCGTAACATA 2131
 QY 3426 TCGTCTTAGTCCAAACCCGTAAGACACGACTTATCGCCACTGSCACAGCCACTGGTAA 3485
 Db 2132 TCGTCTTAGTCCAAACCCGTAAGACACGACTTATCGCCACTGSCACAGCCACTGGTAA 2191
 QY 3486 CAGGATTTAGCAGAGCGATGTAGCGGTGTACAGAGTTCTTGAAGTGGTGGCTAA 3545
 Db 2192 CAGGATTTAGCAGAGCGATGTAGCGGTGTACAGAGTTCTTGAAGTGGTGGCTAA 2251
 QY 3546 CTACGGCTACACTAGAGAACAGTATTTGGTATCTGGCTCTGCTGAGCCAGTTACCTT 3605
 Db 2252 CTACGGCTACACTAGAGAACAGTATTTGGTATCTGGCTCTGCTGAGCCAGTTACCTT 2311
 QY 3606 CGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACCGCTGGTAGCGGTGTT 3665
 Db 2312 CGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACCGCTGGTAGCGGTGTT 2371
 QY 3666 TTTTGTTCGACGACAGATTACGGCGAGAAAAAGGATCTCAAGAGATCTTTGAT 3725
 Db 2372 TTTTGTTCGACGACAGATTACGGCGAGAAAAAGGATCTCAAGAGATCTTTGAT 2431
 QY 3726 CTTTCTACGGGTCTGACGCTCAGTGGAGAACGAAACTCAGTTAAGGATTTTGGTCAT 3785
 Db 2432 CTTTCTACGGGTCTGAG 2449
 QY 3786 GAGATTATCGTCGACAAAGCGGCATCGTGCTCCCACTCTCTGCAGTTTCGGGGCATG 3845
 Db 2450 2449
 QY 3846 GATCGCGGATAGCGCTGCTGGTTCTTGATGCGACGGATTTGCACTGCGCGTAGAA 3905
 Db 2450 2449
 QY 3906 CTCCGGAGGTCTGACGCTCAGGACGAGCTGAACCACTCGCGAGGGATTCAGAGCC 3965
 Db 2450 2449
 QY 3966 GGGGTGGCGAGAACTCCAGCATGAGATCCCGCTGGAGGATCATCCAGCCGGCTC 4025
 Db 2450 2449
 QY 4026 CCGAAAAAGATTCCGAGCCCAACTTTTCATAGAGGCGGCGGTGGAATCGAAATCTCG 4085
 Db 2450 2449

QY 4086 TGATGCGAGGTTGGGCGTCTGCTTGGTCTGGTCAATTTGGAACCCAGAGTCCCGCTCAGAG 4145
 Db 2450 2459
 QY 4146 AACTCGTCAAGAGCGGATAGAGCGGATGCGTCTGGAATCGGAGCGCGCATCCGTAA 4205
 Db 2460 AACTCGTCAAGAGCGGATAGAGCGGATGCGTCTGGAATCGGAGCGCGCATCCGTAA 2519
 QY 4206 AGCAGGAGGAGCGGTAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
 Db 2520 AGCAGGAGGAGGAGCGGTAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCACGGGTAGCC 2579
 QY 4266 AACGCTATGTCTCTGATAGCGGTTCGCGCCACACCCAGCGGCGCACAGTCGATCAATCAGAA 4325
 Db 2580 AACGCTATGTCTCTGATAGCGGTTCGCGCCACACCCAGCGGCGCACAGTCGATCAATCAGAA 2639
 QY 4326 AAGCGGCAATTTCCACCATGATATTGGCAAGCAGGATCGCCATGGGTCAACGACGAGA 4385
 Db 2640 AAGCGGCAATTTCCACCATGATATTGGCAAGCAGGATCGCCATGGGTCAACGACGAGA 2699
 QY 4386 TCCTCGCGGTGGGCGATCGCGCTTCAGCTTGGCGAAACAGTTGGGTGGCGGAGCCCC 4445
 Db 2700 TCCTCGCGGTGGGCGATCGCGCTTCAGCTTGGCGAAACAGTTGGGTGGCGGAGCCCC 2759
 QY 4446 TGATGCTCTTCTGATCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTGCT 4505
 Db 2760 TGATGCTCTTCTGATCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTGCT 2819
 QY 4506 CGCTCGATGCGATGTTTCGCTTGGTTCGAAATGGGCGAGGTAGCGGATCAAGCGTATGC 4565
 Db 2820 CGCTCGATGCGATGTTTCGCTTGGTTCGAAATGGGCGAGGTAGCGGATCAAGCGTATGC 2879
 QY 4566 AGCGCGCGATTCGATCAGCATGAGGATGATCTTCTCGGAGAGCAAGTGTAGATGAC 4625
 Db 2880 AGCGCGCGATTCGATCAGCATGAGGATGATCTTCTCGGAGAGCAAGTGTAGATGAC 2939
 QY 4626 AGGAGATCTCTGCGCCGCACTTCGCGCAATAGCAGCGAGTCCCTTCGCGTCTCAGTGACA 4685
 Db 2940 AGGAGATCTCTGCGCCGCACTTCGCGCAATAGCAGCGAGTCCCTTCGCGTCTCAGTGACA 2999
 QY 4686 ACCTCGACACAGCTCGCAAGGAAACCGCGTCTGGCGAGCCAGCATAGCCGCGTGC 4745
 Db 3000 ACCTCGACACAGCTCGCAAGGAAACCGCGTCTGGCGAGCCAGCATAGCCGCGTGC 3059
 QY 4746 TCGTCTCTGAGTTCATTCAGGCGACCGGACAGGTCTGCTTGAACAAAAACCGGCGC 4805
 Db 3060 TCGTCTCTGAGTTCATTCAGGCGACCGGACAGGTCTGCTTGAACAAAAACCGGCGC 3119
 QY 4806 CCCTGCGCTGACAGCGGAAACACCGCGCATCAGACAGCGCATTCGCTGTTGTCGCGAG 4865
 Db 3120 CCCTGCGCTGACAGCGGAAACACCGCGCATCAGACAGCGCATTCGCTGTTGTCGCGAG 3179
 QY 4866 TCATAGCGGAATAGCTCTTCCACCAAGCGCGGAGAACCTGCGTGAATCATCTTGT 4925
 Db 3180 TCATAGCGGAATAGCTCTTCCACCAAGCGCGGAGAACCTGCGTGAATCATCTTGT 3239
 QY 4926 TCAATCATGCGAAACGATCCTCATCTGCTCTTGAATCAGATCTTGAATCCCTGCGCAT 4985
 Db 3240 TCAATCATGCGAAACGATCCTCATCTGCTCTTGAATCAGATCTTGAATCCCTGCGCAT 3299
 QY 4986 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCGAGGCTTCCCAACCTTACCA 5045
 Db 3300 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCGAGGCTTCCCAACCTTACCA 3359
 QY 5046 GAGGCGCGCGAGTGGCAATTCGCGTTTCGTTTCGTTTCATATAAACCGCCAGTCTAGC 5105
 Db 3360 GAGGCGCGCGAGTGGCAATTCGCGTTTCGTTTCGTTTCATATAAACCGCCAGTCTAGC 3419
 QY 5106 TATCGCCATGTAAGCCCACTCGAAGCTACCTGCTTTCTCTT 5146
 Db 3420 AACTGTTGGGAAGGCGGATCGGTGCGGCTCTTCTGCTATT 3460

QY 4026 CCGGAAACGATTCGGAAGCCAAACCTTTCATAGAGCGCGGTGGAATCGAAATCTCG 4085
 Db 2450 ----- 2449
 QY 4086 TGATGCGAGTTGGCGTCGCTTGTTGCTCAATTCGAAACCCAGAGTCCCGCTCAGAG 4145
 Db 2450 -----CGTCAAGAG 2459
 QY 4146 AACTCGTCAAGAGCGGATAGAGGGGATGCGCTCGGAATCGGGAGCGCGATACCGTAA 4205
 Db 2460 AACTCGTCAAGAGCGGATAGAGGGGATGCGCTCGGAATCGGGAGCGCGATACCGTAA 2519
 QY 4206 AGCAGAGAGCGGTGAGCCCATTCGCGCAAGCTCTTCAGCAATATCAGGGTAGCC 4265
 Db 2520 AGCAGAGAGCGGTGAGCCCATTCGCGCAAGCTCTTCAGCAATATCAGGGTAGCC 2579
 QY 4266 AACGCTATGCTGATAGCGGTTCGCCACACCCAGCGGCCACAGTTCGATGAATCCAGAA 4325
 Db 2580 AACGCTATGCTGATAGCGGTTCGCCACACCCAGCGGCCACAGTTCGATGAATCCAGAA 2639
 QY 4326 AAGCGGCCATTTCCACCATGATATTCGCAAGCAGGATGCCATGGGTCAAGCAGAGA 4385
 Db 2640 AAGCGGCCATTTCCACCATGATATTCGCAAGCAGGATGCCATGGGTCAAGCAGAGA 2699
 QY 4386 TCCTCGCGCTCGGCGATCGCGCTTGAGCCTGGCGACAGTTCGGCTGGCGGAGCCCC 4445
 Db 2700 TCCTCGCGCTCGGCGATCGCGCTTGAGCCTGGCGACAGTTCGGCTGGCGGAGCCCC 2759
 QY 4446 TGATGCTCTTGGTCAAGATCATCTGATCGCAAGACCGGCTTCATCCGAGTAGCTGCT 4505
 Db 2760 TGATGCTCTTGGTCAAGATCATCTGATCGCAAGACCGGCTTCATCCGAGTAGCTGCT 2819
 QY 4506 CGCTCGATGCGATGTTTCGCTTGGTGGTTCGATGCGGAGGTAGCGGATCAAGGTTATGC 4565
 Db 2820 CGCTCGATGCGATGTTTCGCTTGGTGGTTCGATGCGGAGGTAGCGGATCAAGGTTATGC 2879
 QY 4566 AGCGCGCGCTTGGTCAAGATCATCTGATCGCAAGACCGGCTTCATCCGAGTAGCTGCT 4625
 Db 2880 AGCGCGCGCTTGGTCAAGATCATCTGATCGCAAGACCGGCTTCATCCGAGTAGCTGCT 2939
 QY 4626 AGAGATCTTGGCGCGCACTTCGCCCAATAGCAGCGAGTCCCTTCGCGCTTCAGTGACA 4685
 Db 2940 AGAGATCTTGGCGCGCACTTCGCCCAATAGCAGCGAGTCCCTTCGCGCTTCAGTGACA 2999
 QY 4686 ACCTCGAGCACAGTCCGCGAGAAACCCCGTGTGGCCAGCCAGATAGCGCGTGC 4745
 Db 3000 ACCTCGAGCACAGTCCGCGAGAAACCCCGTGTGGCCAGCCAGATAGCGCGTGC 3059
 QY 4746 TCCTCTGCGAGTTCAITTCAGGGCACCGGACAGTTCGCTCTTGACAAAGAAACCGGGCGC 4805
 Db 3060 TCCTCTGCGAGTTCAITTCAGGGCACCGGACAGTTCGCTCTTGACAAAGAAACCGGGCGC 3119
 QY 4806 CCTGCGCTGACAGCGGAAACCGGCGGATCAGAGCAGCGGATTCGCTCTTGCGCCAG 4865
 Db 3120 CCTGCGCTGACAGCGGAAACCGGCGGATCAGAGCAGCGGATTCGCTCTTGCGCCAG 3179
 QY 4866 TCATAGCCGAATAGCTTCCACCCAGCGCGGAGAACCTGCGTCAATCCATCTTGT 4925
 Db 3180 TCATAGCCGAATAGCTTCCACCCAGCGCGGAGAACCTGCGTCAATCCATCTTGT 3239
 QY 4926 TCAATCATCGAAAGATCTCTCTCTCTGATCAGATCTTGATCCCTTGGCCAT 4985
 Db 3240 TCAATCATCGAAAGATCTCTCTCTCTGATCAGATCTTGATCCCTTGGCCAT 3299
 QY 4986 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACCTTTGCGAGGCTTCCCAACCTTACCA 5045
 Db 3300 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACCTTTGCGAGGCTTCCCAACCTTACCA 3359
 QY 5046 GAGGCGCCCGAGCTGGCAATTCGGGTTCGCTGCTGCTCCATATAACCGCCAGTCTAGC 5105
 Db 3360 GAGGCGCCCGAGCTGGCAATTCGGGTTCGCTGCTGCTCCATATAACCGCCAGTCTAGC 3419
 QY 5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTCTCTT 5146

Db 3420 AACTGTTGGAGGGCGATCGGTGGCGGCTCTTCGCTATT 3460

RESULT 13
AAL62059

XX AAL62059 standard; DNA; 3534 BP.

XX AAL62059;

DT 22-SEP-2003 (first entry)

XX TI-GHRH plasmid DNA.

XX Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;
 KW sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;
 KW lymphoma; weight loss; lymphopoeisis; appetite stimulant; anorectic;
 KW growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.

OS Unidentified.

XX WO2003049700-A2.

XX 19-JUN-2003.

PF 10-DEC-2002; 2002WO-US039509.

XX 11-DEC-2001; 2001US-0339610P.

XX (ADVI-) ADVISYS INC.

PA (BAY) BAYLOR COLLEGE MEDICINE.

XX Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;
 PI Hahn K, Brenner MK;

XX WPI; 2003-558968/52.

XX Treating anemia, immune dysfunction, tumor, increasing total red blood
 cell mass, reversing wasting or abnormal weight loss in subject, by
 PT administering nucleic acid construct encoding growth-hormone-releasing-
 hormone.

XX Claim 4; Page 191-193; 212pp; English.

XX The invention relates to compositions and methods for plasmid-mediated
 CC supplementation. The method is useful for treating anaemia, tumour (such
 CC as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
 CC dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
 CC kidney failure, for preventing the development of metastatic tumour, for
 CC increasing total red blood cell mass, for reversing wasting, abnormal
 CC weight loss or suppression of lymphopoeisis, in a subject, or for
 CC increasing weight gain in a chronically ill subject or, or for extending
 CC life expectancy for a chronically ill subject. The present sequence is TI
 CC -growth hormone releasing hormone (GHRH) plasmid DNA. This sequence is
 CC used to illustrate the method of the invention

XX Sequence 3534 BP; 764 A; 1017 C; 978 G; 775 T; 0 U; 0 Other;

Query Match

Best Local Similarity 30.4%; Score 1603.8; DB 8; Length 3534;

Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY 2706 CTAGACGTAATCATGCTATAGCTGTTTCTGTTGAAATTTATCCGCTCACAAATTC 2765

Db 1412 CTGCGGTAATCATGCTATAGCTGTTTCTGTTGAAATTTATCCGCTCACAAATTC 1471

QY 2766 ACACAAATACGAGCGGAGCATAAAGTGAAGCCTGGGTGCTATAGTAGAGCTA 2825

Db 1472 ACACAAATACGAGCGGAGCATAAAGTGAAGCCTGGGTGCTATAGTAGAGCTA 1531

QY 2826 ACTCACATTAATTCGTTGCGCTCACTCCCGCTTTCAGTCGGGAAACCTGTCGTGCCA 2885

Db 1532 ACTCACATTAATTCGTTGCGCTCACTCCCGCTTTCAGTCGGGAAACCTGTCGTGCCA 1591

Db 3360 GAGGCGCCCGAGCTGGCAATTCGGTTGCTTGTCTGTCCATAAAACCGCCAGTCTAGC 3419
 QY 5106 TATCGCATGTAAAGCCCACTGAAGCTACTGCTTCTCTT 5146
 Db 3420 AACTGTGGAAAGGCGATCGGTGCGGCGCTCTTCGCTATT 3460

RESULT 14
 AAL62058
 ID AAL62058 standard; DNA; 3534 BP.
 AC AAL62058;
 XX
 DT 22-SEP-2003 (first entry)
 XX
 DE PSP-HV-GHRH plasmid DNA.
 XX
 KW Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;
 KW sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;
 KW lymphoma; weight loss; lymphopoesis; appetite stimulant; anorectic;
 KW growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.
 XX
 OS Unidentified.
 XX
 PN WO2003049700-A2.
 XX
 PD 19-JUN-2003.
 XX
 PF 10-DEC-2002; 2002WO-US039509.
 XX
 PR 11-DEC-2001; 2001US-0339610P.
 XX
 PA (ADVI-) ADVISYS INC.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;
 PI Hahn K, Brenner MK;
 XX
 PI WPI; 2003-558968/52.
 XX
 PT Treating anemia, immune dysfunction, tumor, increasing total red blood
 PT cell mass, reversing wasting or abnormal weight loss in subject, by
 PT administering nucleic acid construct encoding growth-hormone-releasing-
 XX hormone.
 PS Claim 4; Page 189-191; 212pp; English.
 XX
 CC The invention relates to compositions and methods for plasmid-mediated
 CC supplementation. The method is useful for treating anaemia, tumour (such
 CC as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
 CC dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
 CC kidney failure, for preventing the development of metastatic tumour, for
 CC increasing total red blood cell mass, for reversing wasting, abnormal
 CC weight loss or suppression of lymphopoesis, in a subject, or for
 CC increasing weight gain in a chronically ill subject, or for extending
 CC life expectancy for a chronically ill subject. The present sequence is
 CC PSP-HV-growth hormone releasing hormone (GHRH) plasmid DNA. This sequence
 CC is used to illustrate the method of the invention
 XX
 SQ Sequence 3534 BP; 764 A; 1018 C; 979 G; 773 T; 0 U; 0 Other;

Query Match 30.4%; Score 1603.8; DB 8; Length 3534;
 Best Local Similarity 82.8%; Pred. No. 1.8e-234;
 Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY 2706 CTAGAGCTAATCATGTCTAGTCTTCCCTGTGTGAATTTATCCCTCACAATTC 2765
 Db 1412 CTGGGTAAATCATGGTCATAGCTGTTCCTGTGAAATTTATCCCTCACAATTC 1471
 QY 2766 ACACAACATACGAGCGGAAGCATAAAGTGTAAAGCTGGGTGCTTATGATGAGCTA 2825
 Db 1472 ACACAACATACGAGCGGAAGCATAAAGTGTAAAGCTGGGTGCTTATGATGAGCTA 1531

QY 2826 ACTCATTAAATGCGTTGCGCTCACTGCCCGTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
 Db 1532 ACTCATTAAATGCGTTGCGCTCACTGCCCGTTTCCAGTCGGGAAACCTGTCGTGCCA 1591
 QY 2886 GCTGATTAAATGCGGCAACGCGCGGGAGAGCGGTTTTCGCTATTTGGGGGCTCTTC 2945
 Db 1592 GCTGATTAAATGCGGCAACGCGCGGGAGAGCGGTTTTCGCTATTTGGGGGCTCTTC 1651
 QY 2946 CGCTTCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3005
 Db 1652 CGCTTCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 1711
 QY 3006 TCACTCAAAGGCGTAATACGTTTATCCACAGATTCAGGGGATTAACGAGGAAAGAAAT 3065
 Db 1712 TCACTCAAAGGCGTAATACGTTTATCCACAGATTCAGGGGATTAACGAGGAAAGAAAT 1771
 QY 3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCC 3125
 Db 1772 GTGAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCC 1831
 QY 3126 CCATAGGCTCCGCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGCG 3185
 Db 1832 CCATAGGCTCCGCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGCG 1891
 QY 3186 AAACCCGACAGGACTATAAGATACAGGCGTTTCCCTCGGAAAGTCCCTCGTGGCTC 3245
 Db 1892 AAACCCGACAGGACTATAAGATACAGGCGTTTCCCTCGGAAAGTCCCTCGTGGCTC 1951
 QY 3246 TCCTGTTCCGACCTCGCGCTTACGGGATACCTGCGGCTTACGGGATACCTGCGGCTT 2011
 Db 1952 TCCTGTTCCGACCTCGCGCTTACGGGATACCTGCGGCTTACGGGATACCTGCGGCTT 2071
 QY 3306 GCGCTTTCTCATAGCTCAAGCTAGCTATCTCAGTTGCGTGTAGTGTGCTGCTCAA 3365
 Db 2012 GCGCTTTCTCATAGCTCAAGCTAGCTATCTCAGTTGCGTGTAGTGTGCTGCTCAA 2071
 QY 3366 GCTGGGCTGTGCACGAAACCCCGCTTACGCGGACCCGCTGCGCTTATCCGTAAC 3425
 Db 2072 GCTGGGCTGTGCACGAAACCCCGCTTACGCGGACCCGCTGCGCTTATCCGTAAC 2131
 QY 3426 TCCTGTTGAGTCCAAACCCCGCTTACGCGGACCCGCTGCGCTTATCCGTAAC 3485
 Db 2132 TCCTGTTGAGTCCAAACCCCGCTTACGCGGACCCGCTGCGCTTATCCGTAAC 2191
 QY 3486 CAGATTAGCAGAGGAGTATGAGCGGTGTACAGAGTTCTTGAAGTGGTGGCTAA 3545
 Db 2192 CAGATTAGCAGAGGAGTATGAGCGGTGTACAGAGTTCTTGAAGTGGTGGCTAA 2251
 QY 3546 CTACGGCTACCTAGAGACAGTATTTGGTATCTGGCTCTGCTGAGCCAGTTACCTT 3605
 Db 2252 CTACGGCTACCTAGAGACAGTATTTGGTATCTGGCTCTGCTGAGCCAGTTACCTT 2311
 QY 3606 CGGAAAGAGTTGTTAGCTCTTGTATCCGCAAAACAAACCCGCTGCTGAGCGGTGTT 3665
 Db 2312 CGGAAAGAGTTGTTAGCTCTTGTATCCGCAAAACAAACCCGCTGCTGAGCGGTGTT 2371
 QY 3666 TTTTGTTCAGAGCAGATTAACGCGCAGAAAAGGATCTCAAGAGATCTTTGAT 3725
 Db 2372 TTTTGTTCAGAGCAGATTAACGCGCAGAAAAGGATCTCAAGAGATCTTTGAT 2431
 QY 3726 CTTTCTACGGGCTGAGCTCAGTGGAGCAAAACCTCACGTTAAGGATTTTGGTCA 3785
 Db 2432 CTTTCTACGGGCTGAGCTCAGTGGAGCAAAACCTCACGTTAAGGATTTTGGTCA 2449
 QY 3786 GAGATTATGTCGACCAAAAGCGGCATCGTGCTCCCACTCTGAGTTTCGGGGCAG 3845
 Db 2450 ----- 2449
 QY 3846 GATGCGGATAGCCGCTGCTGGTTTCTTGGATGCGGAGATTTGCACTGCGGTAGAA 3905
 Db 2450 ----- 2449

3300 CAGATCTTGGCGCAAGAACCATCCAGTTTACTTTGCGGGCTTCCCAACCTTACCA 3359
35046 GAGGGGCCCCAGCTGCAATTCGGTTTCGTTGCTGTCATATAAAGCCGCGCTAGC 5105
3360 GAGGGGCCCCAGCTGCAATTCGGTTTCGTTGCTGTCATATAAAGCCGCGCTAGC 3419
5106 TATGCCATGTAAGCCCACTGCAAGCTACCTGCTTCTCTT 5146
3420 AACTGTTGGGAAGGGGATCGTGGCGGCTCTTCGCTATT 3460
RESULT 15
AAL62061
ID AAL62061 standard; DNA; 3534 BP.
XX AAL62061;
XX 22-SEP-2003 (first entry)
XX 15/27/28-GHRH plasmid DNA.
XX Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;
KW sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;
KW lymphoma; weight loss; lymphopoeisis; appetite stimulant; anorectic;
KW growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.
XX Unidentified.
XX WO2003049700-A2.
XX 19-JUN-2003.
XX 10-DEC-2002; 2002WO-US039509.
XX 11-DEC-2001; 2001US-0339610P.
XX (ADVT-) ADVISYS INC.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX Draghia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;
XX Hahn K, Brenner MK;
XX WPI; 2003-558968/52.
XX Treating anaemia, immune dysfunction, tumor, increasing total red blood
PT cell mass, reversing wasting or abnormal weight loss in subject, by
PT administering nucleic acid construct encoding growth-hormone-releasing-
PT hormone.
XX Claim 4; Page 196-197; 212pp; English.
XX The invention relates to compositions and methods for plasmid-mediated
XX supplementation. The method is useful for treating anaemia, tumour (such
XX as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
XX dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
XX kidney failure, for preventing the development of metastatic tumour, for
XX increasing total red blood cell mass, for reversing wasting, abnormal
XX weight loss or suppression of lymphopoeisis, in a subject, or for
XX increasing weight gain in a chronically ill subject or, or for extending
XX life expectancy for a chronically ill subject. The present sequence is
XX 15/27/28-growth hormone releasing hormone (GHRH) plasmid DNA. This
XX sequence is used to illustrate the method of the invention
XX Sequence 3534 BP; 764 A; 1017 C; 978 G; 775 T; 0 U; 0 Other;
Query Match 30.4%; Score 1603.8; DB 8; Length 3534;
Best Local Similarity 82.8%; Pred. No. 1.8e-234; Indels 392; Gaps 1;
Matches 2022; Conservative 0; Mismatches 27;
QY 2706 CTAGACGTAATCATGGTCATAGCTTTTCTGTTGTAATTTTATCCGCTCACATTC 2765
DB 1412 CTGGCGTAATCATGGTCATAGCTTTTCTGTTGTAATTTTATCCGCTCACATTC 1471

3906 CTCGCGAGTGTCTCAGCTCAGCGACAGCTGAAACAACTCGGAGGGGATCGAGCCC 3965
2450 ----- 2449
3966 GGGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGCTC 4025
2450 ----- 2449
4026 CCGGAACAGATTCGGAACCCAACTTTTCATAGAAGCGCGGTGGAATCGAAATCTCG 4085
2450 ----- 2449
4086 TGATGGCAGTTGGCGCTCGCTTGTGCGTCAATTCGAAACCCAGAGTCCCGCTCAGAAG 4145
2450 ----- CGCTCAGAAG 2459
4146 AACTCGTCAAGAGCGGATAGAGGGGATGCGCTCGAATCGGAGCGCGATACCGTAA 4205
2460 AACTCGTCAAGAGCGGATAGAGGGGATGCGCTCGAATCGGAGCGCGATACCGTAA 2519
4206 AGCAGGAGAGCGGTGAGCCCAATTCGCGCCAAAGCTCTTCAGCAATATACGGGTAGCC 4265
2520 AGCAGGAGAGCGGTGAGCCCAATTCGCGCCAAAGCTCTTCAGCAATATACGGGTAGCC 2579
4266 AAGCGTATGCTCTGATAGCGGTGCGCCACACCGAGCGGCCACAGTCGATGATCCAGAA 4325
2580 AAGCGTATGCTCTGATAGCGGTGCGCCACACCGAGCGGCCACAGTCGATGATCCAGAA 2639
4326 AAGCGGCGATTTTCACCATGATATTCGCGCAGCAGCGCATCGCATGGTTCACGACGAGA 4385
2640 AAGCGGCGATTTTCACCATGATATTCGCGCAGCAGCGCATCGCATGGTTCACGACGAGA 2699
4386 TCCTCGCGTTCGCGCATGCGCGCTTGAGCTGCGCAACAGTTTCGCTGCGCGAGCCGCC 4445
2700 TCCTCGCGTTCGCGCATGCGCGCTTGAGCTGCGCAACAGTTTCGCTGCGCGAGCCGCC 2759
4446 TGATGCTCTTCGTCAGATCATCTGATCGAAGACCGGCTTCATCCAGTACGTCT 4505
2760 TGATGCTCTTCGTCAGATCATCTGATCGAAGACCGGCTTCATCCAGTACGTCT 2819
4506 CGCTCGATGCGATTTTCGCTTGGTTCGAAATGGGCGAGTTCGCGCATCAAGGTATGC 4565
2820 CGCTCGATGCGATTTTCGCTTGGTTCGAAATGGGCGAGTAGCCGATCAAGGTATGC 2879
4566 AGCGCGCATTCGATCAGCATCATGATGATATTTCTCGCAGAGCAAGGTGATGAC 4625
2880 AGCGCGCATTCGATCAGCATCATGATGATATTTCTCGCAGAGCAAGGTGATGAC 2939
4626 AGGAGATCTTGGCGCGCATCTTCGCCAATAGCAGCGAGTCCCTTCGCGCTTCAGTGACA 4685
2940 AGGAGATCTTGGCGCGCATCTTCGCCAATAGCAGCGAGTCCCTTCGCGCTTCAGTGACA 2999
4686 ACCTCGAGCAGTTCGCGAGGAGCGCGCTGCTGCGCAGCAGATAGCGCGCTGCC 4745
3000 ACCTCGAGCAGTTCGCGAGGAGCGCGCTGCTGCGCAGCAGATAGCGCGCTGCC 3059
4746 TCGTCTTCGAGTTCATTCAGGGGACCGGACAGGTTCGTTTGAACAAAAGAACCGGGCGC 4805
3060 TCGTCTTCGAGTTCATTCAGGGGACCGGACAGGTTCGTTTGAACAAAAGAACCGGGCGC 3119
4806 CCCTGCGTGAACCGGAAACACGGCGCATCAGAGCGCGATGCTGTTGTCGCCAG 4865
3120 CCCTGCGTGAACCGGAAACACGGCGCATCAGAGCGCGATGCTGTTGTCGCCAG 3179
4866 TCATAGCGGATAGCTCTCCACCAAGCGCGCGGAGAACCTTCGTCGAAATCCATCTTGT 4925
3180 TCATAGCGGATAGCTCTCCACCAAGCGCGCGGAGAACCTTCGTCGAAATCCATCTTGT 3239
4926 TCAATCATGCGAAGACGATCTCATCTGCTCTTGAATGATGATCTTCCCTGCGGCAT 4985
3240 TCAATCATGCGAAGACGATCTCATCTGCTCTTGAATGATGATCTTCCCTGCGGCAT 3299
4986 CAGATCTTGGCGGCGAAGAACCATTCAGTTTACTTTGCGAGGGCTTCCCAACCTTACCA 5045

QY	2766	ACACAACATACGAGCGGGAAGCATAAAGTGTAAAGCTCGGGTGCCCTAATAGTGAAGCTA	2825
Db	1472	ACACAACATACGAGCGGGAAGCATAAAGTGTAAAGCTCGGGTGCCCTAATAGTGAAGCTA	1531
QY	2826	ACTCACTTAATTTGGTTGGCTCACTGCGCCCTTTCCAGTCGGGAACCTCTGTCGCA	2885
Db	1532	ACTCACTTAATTTGGTTGGCTCACTGCGCCCTTTCCAGTCGGGAACCTCTGTCGCA	1591
QY	2886	GCTGCATTAATGAATCGGCGCAACCGCGGGGAGAGCGGTTTTCGTAATTTGGGCGCTCTTC	2945
Db	1592	GCTGCATTAATGAATCGGCGCAACCGCGGGGAGAGCGGTTTTCGTAATTTGGGCGCTCTTC	1651
QY	2946	CGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	3005
Db	1652	CGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	1711
QY	3006	TCACCTCAAAGCGGTAAATACCGTTATCCACAGAAATCAGGGGATTAACGACAGGAAGAACAT	3065
Db	1712	TCACCTCAAAGCGGTAAATACCGTTATCCACAGAAATCAGGGGATTAACGACAGGAAGAACAT	1771
QY	3066	GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTTCGCTGGGCTTTT	3125
Db	1772	GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTTCGCTGGGCTTTT	1831
QY	3126	CCATAGGCTCGCGCCCTCGACGAGCATCAAAATTCGACGCTCAAGTCAGAGGTGGCG	3185
Db	1832	CCATAGGCTCGCGCCCTCGACGAGCATCAAAATTCGACGCTCAAGTCAGAGGTGGCG	1891
QY	3186	AAACCCGACAGGACTATAAAGATACCAAGCGGTTTCCGCCCTGGAAGTCCCTCGTGGCTC	3245
Db	1892	AAACCCGACAGGACTATAAAGATACCAAGCGGTTTCCGCCCTGGAAGTCCCTCGTGGCTC	1951
QY	3246	TCCGTGTTCCGACCTCGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGT	3305
Db	1952	TCCGTGTTCCGACCTCGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGT	2011
QY	3306	GGCGCTTTCTCATAGCTACGCTGTAGTATCTCAGTTTCGCTGAGTGTGCTGCTCAA	3365
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Db	3180	TCATAGCCGAATAGCTCTCCACCCAGCGCGGAGAACCTGCTGCAATCCATCTTGT	3239
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Thu Aug 5 08:55:53 2004

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Qy	5106	TATCGCCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTTT	5146
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Job time : 1981 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:18:10 ; Search time 333 Seconds
(without alignments)
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Perfect score: 5283
Sequence: 1 aagcttgacctatgcgact.....tgagtgttgccgagcgtg 5283

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2240	42.4	8349	4	US-09-186-002-16
2	1793.4	33.9	4800	4	US-09-554-929-1
3	1652.4	31.3	5594	4	US-09-380-190A-29
4	1618.2	30.6	6561	4	US-09-380-190A-30
5	1602.2	30.3	5707	2	US-08-472-809B-8
6	1571.6	29.7	4665	3	US-08-948-378A-7
7	1571.6	29.7	4665	3	US-09-169-425C-7
8	1571.6	29.7	4665	4	US-09-759-960-7
9	1570	29.7	4518	4	US-09-380-190A-26
10	1570	29.7	4886	4	US-09-533-220A-4
11	1570	29.7	6139	2	US-08-751-767A-7
12	1569.8	29.7	4748	4	US-09-796-575-4
13	1569.8	29.7	4992	4	US-09-796-575-5
14	1569.8	29.7	8797	2	US-08-723-306-6
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C	28	1501	28.4	6321	4	US-09-380-190A-17	Sequence 17, Appl
C	29	1501	28.4	6359	4	US-09-380-190A-15	Sequence 15, Appl
C	30	1501	28.4	6891	4	US-09-380-190A-16	Sequence 16, Appl
C	31	1501	28.4	8657	4	US-09-380-190A-14	Sequence 14, Appl
	32	1490.4	28.2	3974	3	US-09-026-343-33	Sequence 33, Appl
	33	1490.4	28.2	3974	3	US-09-042-105-16	Sequence 16, Appl
	34	1490.4	28.2	3974	3	US-09-044-856A-7	Sequence 7, Appl
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	37	1490.4	28.2	3974	3	US-09-078-670-4	Sequence 4, Appl
	38	1490.4	28.2	3974	4	US-09-026-408-14	Sequence 14, Appl
	39	1490.4	28.2	3974	4	US-09-362-871-33	Sequence 33, Appl
	40	1490.4	28.2	3974	4	US-09-627-154-4	Sequence 4, Appl
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	42	1490.4	28.2	3974	4	US-09-437-602-4	Sequence 4, Appl
	43	1490.4	28.2	3974	4	US-09-252-656B-50	Sequence 50, Appl
	44	1490.4	28.2	3974	4	US-09-248-998-147	Sequence 147, Appl
	45	1490.4	28.2	3974	4	US-09-105-470B-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-186-002-16
; Sequence 16, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; TITLE OF INVENTION: delta-Endotoxins
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 8349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3666)..(5573)
; OTHER INFORMATION: completely synthesized
US-09-186-002-16

Query Match	42.4%	Score 2240;	DB 4;	Length 8349;
Best Local Similarity	93.4%	Pred. No. 0;	Mismatches 25;	Indels 144;
Matches 2409;	Conservative 0;			Gaps 1;
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Db 3431 GTACACACGTTTTCGCGGACTGGCTTCTACGTTTCGCTTTCCTTTAGCAGCCCTGC 3372
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Db 3371 GCCCTGAGTGTTCGCGGACGCGTG 3348
RESULT 4
US-09-380-190A-30/c
; Sequence 30, Application US/09380190A
; Patent No. 6410220
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,190A
; FILING DATE: 26-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/03918
; FILING DATE: 28-FEB-98
; ATTORNEY/AGENT INFORMATION:
; NAME: MUEITING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 228.00010201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; LENGTH: 6561 base pairs
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-380-190A-30

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NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/004002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4665 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
IS-Org-169-425C-7

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2y	3068	GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCGCGTTCTCGCGCTTTTCC	3127	
Db	2564	GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCGCGTTCTCGCGCTTTTCC	2505	
Qy	3128	ATAGGCTCCGCCCCCTCACCAGAGATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAA	3187	
Qy	2504	ATAGGCTCCGCCCCCTCACCAGAGATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAA	2445	
Db	3188	ACCGACAGGACTATAAAGATACGAGGCGTTCCCGCTGGAACTCCCTCGTGGCTCTC	3247	
Qy	2444	ACCGACAGGACTATAAAGATACGAGGCGTTCCCGCTGGAACTCCCTCGTGGCTCTC	2385	
Db	3248	CTGTTCCGACCCCTGCGCTTACCGATACCTGTCCGCTTCTCCCTTCGCGAAGCGTGG	3307	
Qy	2384	CTGTTCCGACCCCTGCGCTTACCGATACCTGTCCGCTTCTCCCTTCGCGAAGCGTGG	2325	
Db	3308	CGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCTTCGCTCCAAAGC	3367	
Qy	2324	CGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCTTCGCTCCAAAGC	2265	
Db	3368	TGGGCTGTGTGACGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCCGTAACTATC	3427	
Qy	2264	TGGGCTGTGTGACGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCCGTAACTATC	2205	
Db	3428	GTCTTGGTCCAAACCGGTAAAGACAGACTTATCGCACTGGCAGCAGCACTGGTAAACA	3487	
Qy	2204	GTCTTGGTCCAAACCGGTAAAGACAGACTTATCGCACTGGCAGCAGCACTGGTAAACA	2145	
Db	3488	GGATTAGCAGACGAGGTATGAGCGGTGTACAGATTCTTGAAGTGGTGGCTTAAT	3547	
Qy	2144	GGATTAGCAGACGAGGTATGAGCGGTGTACAGATTCTTGAAGTGGTGGCTTAAT	2085	
Db	3548	ACGGCTACACTAGAAACAGATTTTGGTATCTGGCTCTGTGAGCCAGTTACCTTCG	3607	
Qy	2084	ACGGCTACACTAGAAACAGATTTTGGTATCTGGCTCTGTGAGCCAGTTACCTTCG	2025	
Db	3608	GA AAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCCGCTGTGTAGCGTGGTTTT	3667	
Qy	2024	GA AAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCCGCTGTGTAGCGTGGTTTT	1965	
Db	3668	TTGTTTGCAGACGAGATTACCGCAGAAAAAAGATCTCAAGAAAGATCCCTTTGATCT	3727	
Qy	1964	TTGTTTGCAGACGAGATTACCGCAGAAAAAAGATCTCAAGAAAGATCCCTTTGATCT	1905	
Db	3728	TTTCTACGGGCTGTGACGCTCAGTGGAAACGAAACCTCACGTTAAGGATTTTCGTATGA	3787	
Qy	1904	TTTCTACGGGCTGTGACGCTCAGTGGAAACGAAACCTCACGTTAAGGATTTTCGTATGA	1845	
Db	3788	GATTATCGTCGACAAAGCGGCCATCGTCCCT-----	3819	

Db	1844	GAATATCAAAAGGATCTTACCTAGATCTCTTTAAATTAATAAATGAAGTTTAAATCAA	1785
Qy	3820	-----CCCCACTCTCTGAGTTTCGGGG	3840
Db	1784	TCTAAAGTATATAGTAACCTGAGGCTATGGCAGGCTTGCAGGCTTGGCTG	1725
Qy	3841	GCATGGATGCGCGATACCGCTGCTGGTTCTCTGGATGCCGAGATTTCACATGCCGG	3900
Db	1724	CGAGCCTTGGGCTTCAACCCGAACTTGGGGGTGGGGTGGGAAAGAAAGAAACGCGG	1665
Qy	3901	-----TAGAACTCCGCGAGTCTCCAGCTCAGGCAGCAGCTGAACCAAC	3946
Db	1664	CGTATTGCCCAATAGGGGTCTCGTGGGGTATCGACAGATGCCAGCCTGGGACCGAA	1605
Qy	3947	TCGCGAGGGATCGA-----	3961
Db	1604	CCCCCGTTATGAACAAACGACCCACACAGTGGCTTTTATCTGTCTTTTATTGGCG	1545
Qy	3962	-----GCCCCG	3967
Db	1544	TCATAGCGGGTCTCTCCGTAATGTCTCTCCGTGTTTCAGTTACCTCCCCCTAG	1485
Qy	3968	GGTGGCGAAGAACTCCAGCATAGATCCCGCTGGAGGATCATCCAGCGCGCTCC	4027
Db	1484	GGTGGCGAAGAACTCCAGCATAGATCCCGCTGGAGGATCATCCAGCGCGCTCC	1425
Qy	4028	GGAACAGATTCCGAAGCCCAACCTTTTATAGAAGCGCGGTGGAAATCGAAATCTCGTG	4087
Db	1424	GGAACAGATTCCGAAGCCCAACCTTTTATAGAAGCGCGGTGGAAATCGAAATCTCGTG	1365
Qy	4088	ATGGCAGGTGGCGTTCGTTGGTGGTCAATTCGAAACCCAGAGTCCCGCTCAGAGAA	4147
Db	1364	ATGGCAGGTGGCGTTCGTTGGTGGTCAATTCGAAACCCAGAGTCCCGCTCAGAGAA	1305
Qy	4148	CTCGTCAAGAGCGCATAGAAGCGATCGCTCGAATCGGAGCGCGATACCGTAAAG	4207
Db	1304	CTCGTCAAGAGCGCATAGAAGCGATCGCTCGAATCGGAGCGCGATACCGTAAAG	1245
Qy	4208	CACGAGAGCGGTACGCCCATTCGCGCCCAAGCTCTTACGCAATATCACGGTAGCCAA	4267
Db	1244	CACGAGAGCGGTACGCCCATTCGCGCCCAAGCTCTTACGCAATATCACGGTAGCCAA	1185
Qy	4268	CGCTATGCTCTGATAGCGTCCGCGCACACCGAGCGGCCACAGTCAGTGAATCAGAGAA	4327
Db	1184	CGCTATGCTCTGATAGCGTCCGCGCACACCGAGCGGCCACAGTCAGTGAATCAGAGAA	1125
Qy	4328	GCGGCCATTTCCACCATGATATTCGCGACGAGGATCGCATGGGTACAGCAGAGATC	4387
Db	1124	GCGGCCATTTCCACCATGATATTCGCGACGAGGATCGCATGGGTACAGCAGAGATC	1065
Qy	4388	CTCGCGTTCGGGATGCTCGCTTGGCTTGGCGAAGCAGTTTCGGCTGGCGAGCCCTTG	4447
Db	1064	CTCGCGTTCGGGATGCTCGCTTGGCTTGGCGAAGCAGTTTCGGCTGGCGAGCCCTTG	1005
Qy	4448	ATGCTCTTCGTCCAGATCATCTGATCGAAGAACCGGCTTCATCCAGTACGTGCTCG	4507
Db	1004	ATGCTCTTCGTCCAGATCATCTGATCGAAGAACCGGCTTCATCCAGTACGTGCTCG	945
Qy	4508	CTGATGCGATGTTTCGCTTGGTTCGAATGGCAGGTAGCCGATCAACGCTATGCAG	4567
Db	944	CTGATGCGATGTTTCGCTTGGTTCGAATGGGAGGTAGCCGATCAACGCTATGCAG	885
Qy	4568	CCGCGCATTCGATCAGCCATGATGATCTTCTCGCAGGAGCAAGGTGAGATGACAG	4627
Db	884	CCGCGCATTCGATCAGCCATGATGATCTTCTCGCAGGAGCAAGGTGAGATGACAG	825
Qy	4628	GAGATCTTCCCGGCACTTCGCCCAATAGCAGCGAGTCCCTTCCGCTTCAGTGACAC	4687
Db	824	GAGATCTTCCCGGCACTTCGCCCAATAGCAGCGAGTCCCTTCCGCTTCAGTGACAC	765
Qy	4688	GTGAGACAGCTTGGCGAAGNACGCCGTCTGTGGCCAGCCACGATAGCGCGCTCCCTC	4747

Db 764 GTGAGCAGAGCTGCGCAAGGAAGCCCGTGTGGCCAGCAGATAGCGCGCTGCCTC 705
 QY 4748 GTCTCTGCACTTCAATTCAGGGGACCGGACAGGTGCGTCTTTGACAAAAGAACCGGGGCGCC 4807
 Db 704 GTCTTGCAGTTCATTCAGGGGACCGGACAGGTGCGTCTTTGACAAAAGAACCGGGGCGCC 645
 QY 4808 CTGCGCTGACAGCCCGGAACACAGCGGCGCATCAGAGCAGCGGATGTCTGTGTGCGCCAGTC 4867
 Db 644 CTGCGCTGACAGCCCGGAACACAGCGGCGCATCAGAGCAGCGGATGTCTGTGTGCGCCAGTC 585
 QY 4868 ATAGCGGAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGCATTCATCTGTGTC 4927
 Db 584 ATAGCGGAATAGCTCTCCACCAAGCGCGGAGAACCTGCGTGCATTCATCTGTGTC 525
 QY 4928 AATCATGCGGAACGATCTCATCTCTGTCTCTTGATCAGATCTTG 4971
 Db 524 AATCATGCGGAACGATCTCATCTCTGTCTCTTGATCAGATCTTG 481

RESULT 8
 US-09-759-960-7/c
 ; Sequence 7, Application US/09759960
 ; Patent No., 6582704
 ; GENERAL INFORMATION:
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chiczo, Roman M.
 ; APPLICANT: Collins, Edward J.
 ; APPLICANT: Hedley, Mary Lynn
 ; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09759,960
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/169,425
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fraser, Janis K.
 ; REGISTRATION NUMBER: 34,819
 ; REFERENCE/DOCKET NUMBER: 08191/004002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-542-5070
 ; TELEFAX: 617-543-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4665 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-09-759-960-7

Query Match 29.7%; Score 1571.6; DB 4; Length 4665;
 Best Local Similarity 86.3%; Pred. No. 0;
 Matches 1850; Conservative 0; Mismatches 114; Indels 180; Gaps 3;
 QY 3008 ACTCAAGCGGTAAATACGGTTATCCACAGATACAGGGGATACCGCAGGAAAGACATCT 3067
 Db 2624 AATGATGCGGTAAATACGGTTATCCACAGATACAGGGGATACCGCAGGAAAGACATCT 2565

QY 3068 GAGCAAAAGCGCAGCAAAAGGCCAGGAACCGTTAAAAAGCGCGGTTCGTGGCGTTTTTCC 3127
 Db 2564 GAGCAAAAGCGCAGCAAAAGGCCAGGAACCGTTAAAAAGCGCGGTTCGTGGCGTTTTTCC 2505
 QY 3128 ATAGGCTCCGCGCCCGCTGACAGAGCATCACAAAAATCAGCTCAAGTCAGAGGTGGGAA 3187
 Db 2504 ATAGGCTCCGCGCCCGCTGACAGAGCATCACAAAAATCAGCTCAAGTCAGAGGTGGGAA 2445
 QY 3188 ACCGACAGGACTATAAGATACCAAGGCGTTTCCCGCTGGAAGCTCCCTCGCTGCGCTCTC 3247
 Db 2444 ACCGACAGGACTATAAGATACCAAGGCGTTTCCCGCTGGAAGCTCCCTCGCTGCGCTCTC 2385
 QY 3248 CTGTTCCGACCCCTGCGGTTCACCGATACCTTCGCGCTTCTCCCTTCGGGAAGCGTGG 3307
 Db 2384 CTGTTCCGACCCCTGCGGTTCACCGATACCTTCGCGCTTCTCCCTTCGGGAAGCGTGG 2325
 QY 3308 CGTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGTTGAGTTCGTTCCCTCCAGC 3367
 Db 2324 CGTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGTTGAGTTCGTTCCCTCCAGC 2265
 QY 3368 TGGGCTGTGTCAGCAAGAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGCTAACTATC 3427
 Db 2264 TGGGCTGTGTCAGCAAGAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGCTAACTATC 2205
 QY 3428 GTCTTGAGTCCAAACCCGCTAAGACACAGCTTATCCCACTGGCAGCAGCCTGCTGAACA 3487
 Db 2204 GTCTTGAGTCCAAACCCGCTAAGACACAGCTTATCCCACTGGCAGCAGCCTGCTGAACA 2145
 QY 3488 GGATTAGCAGCGAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCTAACT 3547
 Db 2144 GGATTAGCAGCGAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCTAACT 2085
 QY 3548 ACGCTACACTAGAAAGACAGTATTGGTATCTCGCTCTGCTGAAGCAGCTTACCTTCG 3607
 Db 2084 ACGCTACACTAGAAAGACAGTATTGGTATCTCGCTCTGCTGAAGCAGCTTACCTTCG 2025
 QY 3608 GAAAAAGAGTTGGTAGTCTTGTATCCGCGCAACAAACACCGCTGGTAGCGGTGTTTTT 3667
 Db 2024 GAAAAAGAGTTGGTAGTCTTGTATCCGCGCAACAAACACCGCTGGTAGCGGTGTTTTT 1965
 QY 3668 TTGTTTGAAGCAGCAGATTACGCGCAGAAAAAGGATCTCAAGAAAGATCCCTTTGATCT 3727
 Db 1964 TTGTTTGAAGCAGCAGATTACGCGCAGAAAAAGGATCTCAAGAAAGATCCCTTTGATCT 1905
 QY 3728 TTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCAATGA 3787
 Db 1904 TTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCAATGA 1845
 QY 3788 GATTATCGTCGACCAAGCGCCATCGTGCCT 3819
 Db 1844 GATTATCAAAAAGGATCTTCACTAGATCTTTTAAATTAATAATGAAGTTTAAATCAA 1785
 QY 3820 -----CCCCACTCTCTGACGTTCGCGCCCGACGTTGGCTG 1725
 Db 1784 TCTAAAGTATATAGTAACCTGAGGCTATGCGAGGCGCTGCGCCCGACGTTGGCTG 1725
 QY 3841 GCATGGATGCGGGATAGCGGCTGCTGGTTCTGATGCGCGACGAGATTGCACTGCGCG 3900
 Db 1724 CGAGCCCTGGGCTTTCACCCGAACTTGGGGGTGGGGTGGGAAAGGAAAGAACCGGG 1665
 QY 3901 -----TAGAACTCCGCGAGGTCTCCAGCCTCAGGACGAGCTGAACCAAC 3946
 Db 1664 CGTATGCGCCCAATGGGCTCTCGGTGGGTATCGACAGAGTCCAGCCTCGGACCGAA 1605
 QY 3947 TCGCGAGGGGATCGA----- 3961
 Db 1604 CCGCGGTTTATGACAAACAGCACCACACCGTGGTGTATTTCTGCTCTTTTATTTGCGG 1545
 QY 3962 -----GCCCG 3967
 Db 1544 TCATAGCGGGTTCCTTCGGGTATTGTCTCCTTCGGTGTTCAGTTAGCTCCCTCCCTAG 1485

GENERAL INFORMATION:
APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF

NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MINNESOTA
COUNTRY: USA
ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,190A
FILING DATE: 26-Aug-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/03918
FILING DATE: 28-FEB-98
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 228.00010201
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-380-190A-26

Query Match 29.7%; Score 1570; DB 4; Length 4518;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;

QY	3968	GGTGGCGAAGAACTCCAGCATGATCCCGCGCTGGAGGATCATCAGCGCGGTCC	4027
Db	1484	GGTGGCGAAGAACTCCAGCATGATCCCGCGCTGGAGGATCATCAGCGCGGTCC	1425
QY	4028	GGAAACGATTCGAAAGCCCAACCTTTCTATAGAGCGCGGTGAATCGAAATCTCGTG	4087
Db	1424	GGAAACGATTCGAAAGCCCAACCTTTCTATAGAGCGCGGTGAATCGAAATCTCGTG	1365
QY	4088	ATGGCAGCTGGCGTCCCTTGGTCGCTCATTTGAAACCCAGAGTCCCGTTCAGAGAA	4147
Db	1364	ATGGCAGCTGGCGTCCCTTGGTCGCTCATTTGAAACCCAGAGTCCCGTTCAGAGAA	1305
QY	4148	CTCGTCAAGAGCGCATAGAGCGCATGGCTTCCGAATCGGAGCGCGGATACCGTAAAG	4207
Db	1304	CTCGTCAAGAGCGCATAGAGCGCATGGCTTCCGAATCGGAGCGCGGATACCGTAAAG	1245
QY	4208	CACGAGGAGCGGTGAGCCCATTCGCGCGACGCTCTTCAGCAATATCACGGGTAGCCAA	4267
Db	1244	CACGAGGAGCGGTGAGCCCATTCGCGCGACGCTCTTCAGCAATATCACGGGTAGCCAA	1185
QY	4268	CGCTATGCTCATAGCGGTCCGCCACACCCAGCGCGCCACAGTTCGATGAATCCAGAAA	4327
Db	1184	CGCTATGCTCATAGCGGTCCGCCACACCCAGCGCGCCACAGTTCGATGAATCCAGAAA	1125
QY	4328	GCGGCCATTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTACGACGAGATC	4387
Db	1124	GCGGCCATTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTACGACGAGATC	1065
QY	4388	CTGCGCGTGGGATCGCGGCTTGAGCTGGGACAGTTCGGCTGGCGGAGCCCTTG	4447
Db	1064	CTGCGCGTGGGATCGCGGCTTGAGCTGGGACAGTTCGGCTGGCGGAGCCCTTG	1005
QY	4448	ATGCTCTGCTGCAGATCATCTGATCGACAAGACCGGCTTCATCCGAGTACGTGCTCG	4507
Db	1004	ATGCTCTGCTGCAGATCATCTGATCGACAAGACCGGCTTCATCCGAGTACGTGCTCG	945
QY	4508	CTCGATCGGATGTTTGGTGGTTCGAATGGCGAGGTAGCCGGATCAAGCGTATGCAG	4567
Db	944	CTCGATCGGATGTTTGGTGGTTCGAATGGCGAGGTAGCCGGATCAAGCGTATGCAG	885
QY	4568	CGCGCGATTCGATCAGCATGATGATCTTTCTGGCAGGAGCAAGTGAATGACAG	4627
Db	884	CGCGCGATTCGATCAGCATGATGATCTTTCTGGCAGGAGCAAGTGAATGACAG	825
QY	4628	GAGATCTGCGCGGATCTTCGCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAC	4687
Db	824	GAGATCTGCGCGGATCTTCGCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAC	765
QY	4688	GTGAGCACAGCTGCGCAAGAAACGCGCGTGTGGCCAGCCACGATAGCCGCGTGCCTC	4747
Db	764	GTGAGCACAGCTGCGCAAGAAACGCGCGTGTGGCCAGCCACGATAGCCGCGTGCCTC	705
QY	4748	GTCTGAGTTCATTCAGGGCACCGGACAGTTCGCTTTGACAAAAGAACCGGCGGCC	4807
Db	704	GTCTGAGTTCATTCAGGGCACCGGACAGTTCGCTTTGACAAAAGAACCGGCGGCC	645
QY	4808	CTGGCTGACAGCGCGGAACACGCGGCGATCAGACAGCCGATGTCTGTGTGCGCCAGTC	4867
Db	644	CTGGCTGACAGCGCGGAACACGCGGCGATCAGACAGCCGATGTCTGTGTGCGCCAGTC	585
QY	4868	ATAGCCGATAGCTCTCCACCGCAGCGCGGAGAACCTCGGTGCAATCCATCTGTTC	4927
Db	584	ATAGCCGATAGCTCTCCACCGCAGCGCGGAGAACCTCGGTGCAATCCATCTGTTC	525
QY	4928	AATCATGCGGAACGATCTCTATCTCTGTCTTGATCAGATCTTG 4971	
Db	524	AATCATGCGGAACGATCTCTATCTCTGTCTTGATCAGATCTTG 481	

QY	3428	GTCTTGAGTCCAAACCGGTAAACACAGACTTATCGCCACTGCGACGACCACTGGTAACA	3487
Db	2315	GTCTTGAGTCCAAACCGGTAAACACAGACTTATCGCCACTGCGACGACCACTGGTAACA	2374
QY	3488	GGATTAGCAGACGAGGTATGTAGCGGGTGTACAGAGTTCTTGAAGTGTGGCCTAACT	3547
Db	2375	GGATTAGCAGACGAGGTATGTAGCGGGTGTACAGAGTTCTTGAAGTGTGGCCTAACT	2434
QY	3548	ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTCTCTCAAGCCAGTTACCTTCG	3607
Db	2435	ACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTCTCTCAAGCCAGTTACCTTCG	2494
QY	3608	GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACACCGCTGTGTAGCGGTGGTTTTT	3667
Db	2495	GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACACCGCTGTGTAGCGGTGGTTTTT	2554
QY	3668	TTGTTTGAAGCAGCAGAGTATACGGCAGAAAAAAGGATCTCAAGAAGATCCCTTTGATCT	3727
Db	2555	TTGTTTGAAGCAGCAGAGTATACGGCAGAAAAAAGGATCTCAAGAAGATCCCTTTGATCT	2614
QY	3728	TTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGATTTTGGTCATGA	3787
Db	2615	TTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGATTTTGGTCATGA	2674
QY	3788	GATTATCGTCCACCAAGCGGCCATCGTGCT	3819
Db	2675	GATTATCAAAAAGGATCTTCACTAGATCTCTTTTAAATTAATAAGATTTTAAATCAA	2734
QY	3820	-----CCCCACTCTGCGATTGCGGG	3840
Db	2735	TCTAAGTATATATAGTAACTGAGGCTATGGCAGGGCCTGCGGCCGACGTTGGCTG	2794
QY	3841	GCATGGATGCGCGGATACCGCTGCTGGTTCTCTGGATGCCAGCGATTGTCACCTGCCGG	3900
Db	2795	CGAGCCCTGGGCCCTTCAACCGAACTTGGGGGTGGGGTGGGAAAGGAAAGAAACGCGGG	2854
QY	3901	-----TAGAACTCCGCGAGTGTCTCAGCCTCAGGCAGCAGCTGAACCAAC	3946
Db	2855	CGTATGTGCCCCCAATGGGGTCTCGTGGGGTATCGACAGAGTCCAGCCCTGGGCCGAA	2914
QY	3947	TCGCGAGGGGATCGA	3961
Db	2915	CCCCGGTTTATGAACAAACGACCCACACCGTGCCTTTATCTGTCTTTTATTGCGG	2974
QY	3962	-----CCCCGG	3967
Db	2975	TCATAGCGCGGGTTCCTTCGGTATTGTCTCTCTTCGTTTCAGTTAGCTCCCCCTTAG	3034
QY	3968	GGTGGCGAGAACTCCAGATAGATCCCGCGTGGAGGATCATCCAGCGCGCTGCC	4027
Db	3035	GGTGGCGAGAACTCCAGCATAGATCCCGCGTGGAGGATCATCCAGCGCGCTGCC	3094
QY	4028	GGAACAGATTCGGAAGCCCACTTTTCATAGAAGCGCGGTGAATCGAAATCTCGTG	4087
Db	3095	GGAACAGATTCGGAAGCCCACTTTTCATAGAAGCGCGGTGAATCGAAATCTCGTG	3154
QY	4088	ATGGCAGTTGGCGTGTGGTCAATTCGAAACCCAGAGTCCCGCTCAGAAAGAA	4147
Db	3155	ATGGCAGTTGGCGTGTGGTCAATTCGAAACCCAGAGTCCCGCTCAGAAAGAA	3214
QY	4148	CTCGTCAAGAAGCGGATAGAAGGCGATGGCTGCGAATCGGGAGCGGCGATACCGTAAAG	4207
Db	3215	CTCGTCAAGAAGCGGATAGAAGGCGATGGCTGCGAATCGGGAGCGGCGATACCGTAAAG	3274
QY	4208	CACGAGGAACGGGTACGCCCATTCGCCCGCAAGCTCTTCAGCAATATCACGGGTAGCCAA	4267
Db	3275	CACGAGGAACGGGTACGCCCATTCGCCCGCAAGCTCTTCAGCAATATCACGGGTAGCCAA	3334
QY	4268	CGGTATGCTCTGATAGCGGTCCGCACACCCAGCGGCCACAGTCGATGTAATCCAGAAAA	4327
Db	3335	CGGTATGCTCTGATAGCGGTCCGCACACCCAGCGGCCACAGTCGATGTAATCCAGAAAA	3394
QY	4328	GCGGCCATTTTCCACCATGATATTCGGCAAGCGGCAATGCGCATGGGTCCAGCAGATC	4387

Db	3395	GCGCCATTTTCCACCATGATATTCCGCAAGCAGGCATCCGCATGGGTCAACGACGATC	3454
QY	4388	CTCCCGCTCGGGCATCGCGCTTGAGCCTCGCGAACAGTTCGGCTGCGCGAGCCCTTG	4447
Db	3455	CTCGCGCTCGGCATGCTCGCTTGAGCCTGGCGAACAGTTCGGCTGGCGAGCCCTTG	3514
QY	4448	ATGCTCTTCGTCCAGATCATCTGATGCACAAGACCGGCTTCATCCGAGTAGTCTGCTCG	4507
Db	3515	ATGCTCTTCGTCCAGATCATCTGATGCACAAGACCGGCTTCATCCGAGTAGTCTGCTCG	3574
QY	4508	CTCGATCGCATGTTTCGTTGGTGGTGCATGGCGAGGTAGCCGATCAAGCGTATGCAG	4567
Db	3575	CTCGATCGCATGTTTCGTTGGTGGTGCATGGCGAGGTAGCCGATCAAGCGTATGCAG	3634
QY	4568	CCGCGCATTTGCATCAGCCATGATGATATCTTTCTCGCAGGACAAGGTGAGATGCACAG	4627
Db	3635	CCGCGCATTTGCATCAGCCATGATGATATCTTTCTCGCAGGACAAGGTGAGATGCACAG	3694
QY	4628	GAGATCTCTGCCCGGCACCTTCGCCCAATAGCAGCCAGTCCCTTCGCCGTTCAAGTCAAC	4687
Db	3695	GAGATCTCTGCCCGGCACCTTCGCCCAATAGCAGCCAGTCCCTTCGCCGTTCAAGTCAAC	3754
QY	4688	GTGAGCAGAGCTGCGGAGGAAGCCCGCTGTGGCAGCAAGATAGCCGCTGCCTC	4747
Db	3755	GTGAGCAGAGCTGCGGAGGAAGCCCGCTGTGGCAGCAAGATAGCCGCTGCCTC	3814
QY	4748	GTCTCTCAGTTTCATTCCAGGSCACCGACAGGTCTGCTTCGACAAAGAACCGGGCGCC	4807
Db	3815	GTCTCTCAGTTTCATTCCAGGSCACCGACAGGTCTGCTTCGACAAAGAACCGGGCGCC	3874
QY	4808	CTGCGCTGACAGCCGAAACAGCGCGGATCAGAGAGCCGATTGTCTGTTGTGCCAGTC	4867
Db	3875	CTGCGCTGACAGCCGAAACAGCGCGGATCAGAGAGCCGATTGTCTGTTGTGCCAGTC	3934
QY	4868	ATAGCCGAATAGCCTCTCCACCCCAAGCGGCGGAGAACCTTCGTCGAATCCATCTTGTC	4927
Db	3935	ATAGCCGAATAGCCTCTCCACCCCAAGCGGCGGAGAACCTTCGTCGAATCCATCTTGTC	3994
QY	4928	AATCATGCGAACGATCCTCATCTGTCTCTTGATCAGATCTTTG	4971
Db	3995	AATCATGCGAACGATCCTCATCTGTCTCTTGATCAGATCTTTG	4038

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RESULT 10
; US-09-533-220A-4/c
; Sequence 4, Application US/09533220A
; Patent No. 6406908
; GENERAL INFORMATION:
; APPLICANT: McIntyre, Peter
; APPLICANT: James, Iain Fraser
; TITLE OF INVENTION: Human Vanilloid Receptor
; FILE REFERENCE: 4-30875A
; CURRENT APPLICATION NUMBER: US/09/533,220A
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 1.30
; SEQ ID NO 4
; LENGTH: 4886
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-533-220A-4

```

	Query Match	29.7%	Score 1570;	DB 4;	Length 4886;
	Best Local Similarity	86.2%	Pred. No. 0;		
	Matches 1849;	Conservative	0;	Mismatches 115;	Indels 180; Gaps 3;
Qy	3008	ACTCAAAGCGGGTATACGGTTATCCACAGATCAGGGGATAACCGCAGGAAAGAAATGT			3067
Db	4295	AATGCATGCGGGTATACGGTTATCCACAGATCAGGGGATAACCGCAGGAAAGAAATGT			4236

RESULT 11
US-08-751-767A-7/c
; Sequence 7, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:

RESULT 11

APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADORFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6139 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 3222..4841
US-08-751-767A-7

Query Match 29.7%; Score 1570; DB 2; Length 6139;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;
3008 ACTCAAGGGGGTAATACGGTTATCCACAAATCAGGGGTAACGCAAGGAAAGAAACATGT 3067
2624 AATGCATGGCGGTAATACGGTTATCCACAAATCAGGGGTAACGCAAGGAAAGAAACATGT 2565
3068 GAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGGCGCGTTCTGCGCGTTTTC 3127
2564 GAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAGGCGCGTTCTGCGCGTTTTC 2505
3128 ATAGGTCGCGCCCTCGAGAGCATCAAAATCAGAGCTCAAGTCAGAGGTGCGGAA 3187
2504 ATAGGTCGCGCCCTCGAGAGCATCAAAATCAGAGCTCAAGTCAGAGGTGCGGAA 2445
3188 ACCCGACAGACTATTAAGTACCAGCGTTTCCCTCGAGAGCTCCCTCGTGCCTTC 3247
2444 ACCCGACAGACTATTAAGTACCAGCGTTTCCCTCGAGAGCTCCCTCGTGCCTTC 2385
3248 CTGTTCCGACCTCGCGCTTACGGTACCTGTCGCGCTTTCTCCCTTCGGGAGCGTGG 3307
2384 CTGTTCCGACCTCGCGCTTACGGTACCTGTCGCGCTTTCTCCCTTCGGGAGCGTGG 2325
3308 CGCTTCTCATAGTCACTGATCTCAGTTTCGGTTCAGTTCGTTTCGCTCCAGC 3367
2324 CGCTTCTCATAGTCACTGATCTCAGTTTCGGTTCAGTTCGTTTCGCTCCAGC 2265
3368 TGGGCTGTGTACCAAGACCCCGCTTCAGCCGACCGTTCGCGCTTATCCGTAATATC 3427
2264 TGGGCTGTGTACCAAGACCCCGCTTCAGCCGACCGTTCGCGCTTATCCGTAATATC 2205
3428 GTCTTGTAGTCCAAACCCGGTAAAGACAGCACTTATCCGCTGCGCAGGCACTGTTAACA 3487

Db	2204	GTCTTGAGTCCAAACCGGTAAAGACAGACTTATCGCACTGGCAGCAGCACTGTAACA	2145
QY	3488	GGATTAGCAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGTGTCCTAACT	3547
Db	2144	GGATTAGCAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGTGTCCTAACT	2085
QY	3548	ACGGCTACACTAGAAGACAGTATTTGGTATCTGGCTCTGCTGAAGCAGTACCTCG	3607
Db	2084	ACGGCTACACTAGAAGACAGTATTTGGTATCTGGCTCTGCTGAAGCAGTACCTCG	2025
QY	3608	GAAAAAGAGTTGGTAGCTCTTCGATCCGCAAAACACACCGCTGGTAGCGGTGTTTT	3667
Db	2024	GAAAAAGAGTTGGTAGCTCTTCGATCCGCAAAACACACCGCTGGTAGCGGTGTTTT	1965
QY	3668	TTGTTTGAAGCAGAGATTACGGCAGAAAAAGGATCTCAAGAGATCTTTGATCT	3727
Db	1964	TTGTTTGAAGCAGAGATTACGGCAGAAAAAGGATCTCAAGAGATCTTTGATCT	1905
QY	3728	TTTCTACGGGTCTGACGCTCAGTGGAAAGAACTCAGTTAAGGATTTTGGTCATGA	3787
Db	1904	TTTCTACGGGTCTGACGCTCAGTGGAAAGAACTCAGTTAAGGATTTTGGTCATGA	1845
QY	3788	GATTATCGTCGACCAAAAGCGGCATCGTCCT	3819
Db	1844	GATTATCAAAAAGGATCTTACCTAGATCTCTTTAAATTAATAAGTTTTAAATCAA	1785
QY	3820	-----CCCCACTCCTGCAGTTTCGGGG	3840
Db	1784	TCATAAGTATATATGATTAACCTGAGGCTAGGCGGCTTCGCCGCCGAGTTGGTG	1725
QY	3841	GCATGGATGCGGATAGCGCTCTGTTCTCGATGCGCAGCGATTCCTACCTGCGG	3900
Db	1724	CGACCTTGGGCTTTCACCCGAACTTGGGGGTGGGGGAAAGAAAGAAAGCGGG	1665
QY	3901	-----TAGAACTCCGCGAGGTCTCCAGCCTCAGCAGCAGCTGACACCAAC	3946
Db	1664	CGTATTGGCCCCAATGGGTCTCGTGGGTATCGACAGAGTGCACCGCTGGGACCGAA	1605
QY	3947	TCGGAGGGGATCGA	3961
Db	1604	CCCCGCGTTTATGAACAAACGACCAACACCGTGGTTCCTGCTGCTTTTATTCGCG	1545
QY	3962	-----GCCTAGGCTAGCTCCTCCCTAG	1485
Db	1544	TCATAGCGGGTTCCTTCGGTATTTGTCTCTTCGGTTCAGTTAGCTCCTCCCTAG	4027
QY	3968	GTGGCGCAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGCTCC	1425
Db	1484	GTGGCGCAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGCTCC	4087
QY	4028	GGAAACGATTCGAAAGCCCAACTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGT	1424
Db	1424	GGAAACGATTCGAAAGCCCAACTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGT	1365
QY	4088	ATGGCAGTTTGGCGCTCGCTTCGTCATTTTCGAAACCCAGAGTCCGCTCAGAGAA	4147
Db	1364	ATGGCAGTTTGGCGCTCGCTTCGTCATTTTCGAAACCCAGAGTCCGCTCAGAGAA	1305
QY	4148	CTCGTCAAGAGCGCATAGAAGCGATGCGCTGCGAATCGGAGCGCGATACCGTAAAG	4207
Db	1304	CTCGTCAAGAGCGCATAGAAGCGATGCGCTGCGAATCGGAGCGCGATACCGTAAAG	1245
QY	4208	CACGAGGAGCGGTGAGGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCAA	4267
Db	1244	CACGAGGAGCGGTGAGGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCAA	1185
QY	4268	CGCTATGTCCTGATAGCGGTTCGCCACACCGCGCGCAAGTTCGATGAATCCAGAAA	4327
Db	1184	CGCTATGTCCTGATAGCGGTTCGCCACACCGCGCGCAAGTTCGATGAATCCAGAAA	1125
QY	4328	GCGGCCATTTCCACCATGATATTTCGCAAGCAGCATCGCCATCGGTTCAGCAGGATC	4387

Db	1124	CGCGCCATTTTCCACCATGATATTTCGGAAGCAGGATCGCCATCGGTCACGACGATC	1065
Qy	4388	CTCCCGCTCGGCGATCGCGCTTGAGCCTTGGCGAAACAGTTTCGGCTGGCGGAGCCCGCTG	4447
Db	1064	CTCGCGCTCGGCGATGCTCGCTTGAGCCTTGGCGAAACAGTTTCGGCTGGCGGAGCCCGCTG	1005
Qy	4448	ATGCTCTTCGTCACGATCATCTGATCGACAAAGACCGGCTTCATCCGAGTACGTCTCG	4507
Db	1004	ATGCTCTTCGTCACGATCATCTGATCGACAAAGACCGGCTTCATCCGAGTACGTCTCG	945
Qy	4508	CTCGATCGATGTTTCGCTTGGTGTGCAATGGCGAGGTAGCCGATCAAGCTATGCG	4567
Db	944	CTCGATCGATGTTTCGCTTGGTGTGCAATGGCGAGGTAGCCGATCAAGCTATGCG	885
Qy	4568	CGCGCGCATTCGATCAGCAGCATGATGGATCTTCTCGGAGGAGCAAGGTGAGATGAC	4627
Db	884	CGCGCGCATTCGATCAGCAGCATGATGGATCTTCTCGGAGGAGCAAGGTGAGATGAC	825
Qy	4628	GAGATCTCGCCCGGCACTTCGCCAATAGCAGCAGTCCCTTCGCGTTGATGACAC	4687
Db	824	GAGATCTCGCCCGGCACTTCGCCAATAGCAGCAGTCCCTTCGCGTTGATGACAC	765
Qy	4688	GTGAGCAGATGCTGGCAGGAGCAGCCGCTGCTGGCCAGCAGTAGCCGCTGCCTC	4747
Db	764	GTGAGCAGATGCTGGCAGGAGCAGCCGCTGCTGGCCAGCAGTAGCCGCTGCCTC	705
Qy	4748	CTCGCTGAGTTCATTCAGGCGCAGCAGCAGTGGCTTCGCAAAAAGAACCGGCGCC	4807
Db	704	GTCTTGCAGTTTCACTCAGGCGCAGCAGCAGTGGCTTCGCAAAAAGAACCGGCGCC	645
Qy	4808	CTCGCTGAGTTCATTCAGGCGCAGCAGCAGTGGCTTCGCAAAAAGAACCGGCGCC	4867
Db	644	CTCGCTGAGTTCATTCAGGCGCAGCAGCAGTGGCTTCGCAAAAAGAACCGGCGCC	585
Qy	4868	ATAGCGAATAGCTCTCCACCAAGCGCGCGAGAACCTGCTGCAATCCATCTTGTTC	4927
Db	584	ATAGCGAATAGCTCTCCACCAAGCGCGCGAGAACCTGCTGCAATCCATCTTGTTC	525
Qy	4928	AATCATGCGAAGCATCTCATCTGCTCTTGTGATCAGATCTTG	4971
Db	524	AATCATGCGAAGCATCTCATCTGCTCTTGTGATCAGATCTTG	481
RESULT 12			
US-09-796-575-4/c			
; Sequence 4, Application US/09796575			
; Patent No. 6632671			
; GENERAL INFORMATION:			
; APPLICANT: Genesquies, Inc.			
; TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD			
; FILE REFERENCE: G332.12-0001			
; CURRENT APPLICATION NUMBER: US/09/796,575			
; CURRENT FILING DATE: 2001-02-28			
; PRIOR APPLICATION NUMBER: 2000-02-28			
; PRIOR FILING DATE: 2000-02-28			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 4			
; LENGTH: 4748			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Provided by Dr. Brett Levay-Young of the University of Minnesota			
US-09-796-575-4			
Query Match 29.7%; Score 1569.8; DB 4; Length 4748;			
Best Local Similarity 86.3%; Pred. No. 0;			
Matches 1847; Conservative 0; Mismatches 112; Indels 180; Gaps 3;			
Qy	3013	AAGCGGTAATACGGTTATCCACAGATCAGGGGATAACGAGGAAGAAACATGTGAGCA	3072
Db	4744	ATGGCGGTATACGGTTATCCACAGATCAGGGGATAACGAGGAAGAAACATGTGAGCA	4695

3793 TCCTGACCAAGGCGCATGTCCT----- 3819
 4208 TCAAAAGGATCTTCACTAGATCCTTTAAATTAATAAATGAAGTTTAAATCAATCTAA 4149
 3820 -----CCCCACTCTCGAGTTCGGGGCATG 3845
 4148 AGTATATAGTAACTGAGCTATGCGAGGCTGCGGCGCCACGTTGCTGCGAGC 4089
 3846 GATCGGGATAGCGCTGCTGTTCTCTGATGCGGACGAGATTGCACTGCCG----- 3900
 4088 CCGTGGCTTCAACCGAATCTGGGGTGGGGTGGGAAAGGAAAGGAAAGCGCGGAT 4029
 3901 -----TAGAACTCGCGAGTTCGAGCTTCAGCGAGCTGAACCACTCGG 3951
 4028 TGGCCCCAATGGGTCTCGGTGGGTATCGACAGAGTGCAGCCCTGGGACGAAACCCG 3969
 3952 AGGGATCGA----- 3961
 3968 CGTTTATGAACAAACGACCCACACCGTGGTGTATTTCTGCTTTTATTTGCGCTATA 3909
 3962 -----GCCCCGGGTGG 3972
 3908 GCGGGTTCCTTCGGTATTGTTCTCTTCCTTCCTGTTTTCAGTTAGCTCCCTAGGGTGG 3849
 3973 GCGAAGAACTCCAGCATGATGATCCCGCGCTGGAGATCATCCAGCGCGGTCCCGAAA 4032
 3848 GCGAAGAACTCCAGCATGATGATCCCGCGCTGGAGATCATCCAGCGCGGTCCCGAAA 3789
 4033 AGATTCCGAAGCCCACTTTATAGAGGCGCGGTGGAATCGAAATCTCGTATGGC 4092
 3788 AGATTCCGAAGCCCACTTTATAGAGGCGCGGTGGAATCGAAATCTCGTATGGC 3729
 4093 AGTTGGGTGCTGCTTGGTGGTCAATTCGAACCCAGAGTCCCGTCAAGAACTCGT 4152
 3728 AGTTGGGTGCTGCTTGGTGGTCAATTCGAACCCAGAGTCCCGTCAAGAACTCGT 3669
 4153 CAAGAAGGCGATAGAGGCGATCGCTGCGAATCGGGAGCGGCGATACCGTAAGACGA 4212
 3668 CAAGAAGGCGATAGAGGCGATCGCTGCGAATCGGGAGCGGCGATACCGTAAGACGA 3609
 4213 GGAAGCGGTAGCGCATTCGCGCAAGCTCTTCAGCAATATCAGGGTAGCCAAAGCTA 4272
 3608 GGAAGCGGTAGCGCATTCGCGCAAGCTCTTCAGCAATATCAGGGTAGCCAAAGCTA 3549
 4273 TGCTCTGATAGCGGTCCGCCACACCCAGCGGCGACAGTGCATGAATCCAGAAAGCGGC 4332
 3548 TGCTCTGATAGCGGTCCGCCACACCCAGCGGCGACAGTGCATGAATCCAGAAAGCGGC 3489
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 4393 CGTCGGCATCGCGCTTGAGCTGGCAACAGTTCGGTGGCGCGAGCCCTGATGCT 4452
 3428 CGTCGGCATCGCTCGCTTGAGCTGGCAACAGTTCGGTGGCGCGAGCCCTGATGCT 3369
 4453 CTTCGTCCAGATCATCTGATCGAAGACCGGCTTCATCCGAGTAGTCTGCTCGA 4512
 3368 CTTCGTCCAGATCATCTGATCGAAGACCGGCTTCATCCGAGTAGTCTGCTCGA 3309
 4513 TGCATGTTTCTGTTGGTTCGATGGGCGAGTAGCCGATCAAGCGTATGCGCCGCC 4572
 3308 TGCATGTTTCTGTTGGTTCGATGGGCGAGTAGCCGATCAAGCGTATGCGCCGCC 3249
 4573 GCATTGATCAGCCATGATGATCTTTCTGGCAGGAGCAAGGTGAGATGACGAGAT 4632
 3248 GCATTGATCAGCCATGATGATCTTTCTGGCAGGAGCAAGGTGAGATGACGAGAT 3189
 4633 CTGCCCCGGCACTTCGCCAATAGCAGCGAGTCCCTCCCGCTTCAGTGACAAAGTGA 4692
 3188 CTGCCCCGGCACTTCGCCAATAGCAGCGAGTCCCTCCCGCTTCAGTGACAAAGTGA 3129
 4693 GCACAGCTCGCAAGGAGCCCGTCTGGCCAGCCACGATAGCGCGCTGCTCTGCTCT 4752

Db 3128 GCACAGCTCGCAAGGAGCCCGTCTGGCCAGCCACGATAGCGCGCTGCTCTGCTCT 3069
 Qy 4753 GCAGTTTCAATTCAGGCGACCGGACAGTTCGTTTGAACAAAAGAACCGGGCGCCCTCGC 4812
 Db 3068 GCAGTTTCAATTCAGGCGACCGGACAGTTCGTTTGAACAAAAGAACCGGGCGCCCTCGC 3009
 Qy 4813 CTGACAGCGGAAACACCGGCGCATCAGAGAGCGGATTCGTTGTGCCAGTCAATAGC 4872
 Db 3008 CTGACAGCGGAAACACCGGCGCATCAGAGAGCGGATTCGTTGTGCCAGTCAATAGC 2949
 Qy 4873 CGAATAGCTCTCAACCAAGCGGCGCGGAGAACCTGCGTGAATCAATCAATCTTGTTCATCA 4932
 Db 2948 CGAATAGCTCTCAACCAAGCGGCGCGGAGAACCTGCGTGAATCAATCAATCTTGTTCATCA 2889
 Qy 4933 TCGCAAGAGATCCTCATCTGCTCTTGTGATCAGATCTTG 4971
 Db 2888 TCGCAAGAGATCCTCATCTGCTCTTGTGATCAGATCTTG 2850

RESULT 14
 US-08-723-306-6/c
 ; Sequence 6, Application US/08723306
 ; Patent No. 5856178
 ; GENERAL INFORMATION:
 ; APPLICANT: White PhD, Kenneth
 ; APPLICANT: Morrey PhD, John
 ; APPLICANT: Reed, William
 ; TITLE OF INVENTION: Cassette for Expression of Lytic
 ; TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Trask Britt and Rossa
 ; STREET: P.O. Box 2550
 ; CITY: Salt Lake City
 ; STATE: Utah
 ; COUNTRY: USA
 ; ZIP: 84110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/723,306
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sweigert PhD, Susan E
 ; REGISTRATION NUMBER: 36,289
 ; REFERENCE/DOCKET NUMBER: 2549
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 8015321922
 ; TELEFAX: 8015319168
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8797 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "Construct comprising Bos
 ; DESCRIPTION: taurus beta casein 5' regulatory region plus genes encoding
 ; DESCRIPTION: amphipathic peptide and green fluorescent protein"
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: NO
 ; US-08-723-306-6

Query Match 29.7%; Score 1569.8; DB 2; Length 8797;
 Best Local Similarity 86.3%; Pred. No. 0;
 Matches 1847; Conservative 0; Mismatches 112; Indels 180; Gaps 3;
 QY 3013 AMGGCGGTAAATACGCTTATCCACAGATCAGGGGATAACGAGGAAACATGTGAGCA 3072

Db 8793 ATGGCGGTAATACGGTTATCCACAGATCAGGGATAACGAGGAAGAACATGTGAGCA 8734
QY 3073 AAAGCCAGCAAAAGGCGAGAACCGTAAAAAGGCGCGTTGCTGGCGTTTTCATAGG 3132
Db 8733 AAAGCCAGCAAAAGGCGAGAACCGTAAAAAGGCGCGTTGCTGGCGTTTTCATAGG 8674
QY 3133 CTCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGGGAACCCG 3192
Db 8673 CTCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGGGAACCCG 8614
QY 3193 ACAGGACTATAAGATACACAGCGCTTCCCTGGAAGCTCCCTCGCGCTCTCTGTT 3252
Db 8613 ACAGGACTATAAGATACACAGCGCTTCCCTGGAAGCTCCCTCGCGCTCTCTGTT 8554
QY 3253 CGAGCCCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGTT 3312
Db 8553 CGAGCCCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGTT 8494
QY 3313 TCTCATAGCTCAGCGTGTAGGTATCTCAGTTTCGGTGTAGGTGCTTCCTCAAGCTGGC 3372
Db 8493 TCTCATAGCTCAGCGTGTAGGTATCTCAGTTTCGGTGTAGGTGCTTCCTCAAGCTGGC 8434
QY 3373 TGTGTGACGAACCCCGTTTTCAGCCGACCGCTCGCGCTTATCCGGTAACTATCGTCT 3432
Db 8433 TGTGTGACGAACCCCGTTTTCAGCCGACCGCTCGCGCTTATCCGGTAACTATCGTCT 8374
QY 3433 GAGTCCAAACCCGGTAAGACAGCTTATCGCACTGGCAGAGCCACTGGTAACAGGATT 3492
Db 8373 GAGTCCAAACCCGGTAAGACAGCTTATCGCACTGGCAGAGCCACTGGTAAACAGGATT 8314
QY 3493 AGCAGAGCGAGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTTAACTACGGC 3552
Db 8313 AGCAGAGCGAGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTTAACTACGGC 8254
QY 3553 TACACTAGAAGAACAGTATTTGGTATCTCGCTCTGTGTGAAGCAGTTTACCTTCGGAATA 3612
Db 8253 TACACTAGAAGAACAGTATTTGGTATCTCGCTCTGTGTGAAGCAGTTTACCTTCGGAATA 8194
QY 3613 AGAGTTGGTGTAGCTTGTATCGGCAAAACAAACCCGCTGGTAGCGGTGGTTTTTGT 3672
Db 8193 AGAGTTGGTGTAGCTTGTATCGGCAAAACAAACCCGCTGGTAGCGGTGGTTTTTGT 8134
QY 3673 TGCAAGCAGCAGATTACCGCAGAAAAAAGGATCTCAAGAATCTTTGATCTTTTCT 3732
Db 8133 TGCAAGCAGCAGATTACCGCAGAAAAAAGGATCTCAAGAATCTTTGATCTTTTCT 8074
QY 3733 ACGGGTCTGACGCTCAGTGGAAACGAAACTCAGTTTAAAGGATTTTGGTCATGAGTTA 3792
Db 8073 ACGGGTCTGACGCTCAGTGGAAACGAAACTCAGTTTAAAGGATTTTGGTCATGAGTTA 8014
QY 3793 TCGTGCACAAAGCGGCATCGTGGCT----- 3819
Db 8013 TCAAAAAGGATCTTCACTAGATCTTTTAAATTAATAATGAAGTTTAAATCAATCTAA 7954
QY 3820 ----- 3845
Db 7953 AGTATATATGAGTAACTGAGGCTATGGCAGGCTTGCAGGCTTGGCTGGGAGC 7894
QY 3846 GATCGCGGATACCGGTGTGTTTCTGGATGCGCAGGATTTGCACTGCGG----- 3900
Db 7893 CTTGGCCCTTCAACCGAATTTGGGGGTGGGTGGGGAAGAAAGAACCGGGCGTAT 7834
QY 3901 -----TAGAATCCCGAGGTCTGTCAGCTCAGGAGCAGTGAACCAACTCGCG 3951
Db 7833 TGGCCCAATGGGGTCTCGTGGGGTATCGACAGAGTGGCCCTGGGACCGAACCCCG 7774
QY 3952 AGGGATCGA----- 3961
Db 7773 CGTTTATGAACAAACGACCCAAACCGTGGTTTTTATCTGTTTATTTGCGGTCA 7714
QY 3962 -----GCCCGGGTGG 3972

7713 GCGCGGTTCCCTTCGGTATTCTCTCTTCCCTTCAGTTAGCTCCCTCCTAGGTGG 7654
3973 GCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGATCATCAGCCGCGTCCCGGAAA 4032
7653 GCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGATCATCAGCCGCGTCCCGGAAA 7594
4033 ACGATTCCGAAGCCCAACCTTTATAGAGGCGCGGTGGAAATCGAAATCTCGTGTGGC 4092
7593 ACGATTCCGAAGCCCAACCTTTATAGAGGCGCGGTGGAAATCGAAATCTCGTGTGGC 7534
4093 AGTTTGGCGTGGCTTGGTTCGTCATTTTCGAACCCAGAGTCCCGCTCAGAAGAACTCGT 4152
7533 AGTTTGGCGTGGCTTGGTTCGTCATTTTCGAACCCAGAGTCCCGCTCAGAAGAACTCGT 7474
4153 CAAGAAGCGGATAGAGGCGGATCGCTCGGAATCGGGAGCGCGATACCGTAAAGCAAGA 4212
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4213 GGAAGCGGTACAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGGTAGCCACGCTA 4272
7413 GGAAGCGGTACAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGGTAGCCACGCTA 7354
4273 TGTCTGTATAGCGTTCGCCACACCCAGCCGCGCACAGTTCGATGAATCCAGAAAGCGCG 4332
7353 TGTCTGTATAGCGTTCGCCACACCCAGCCGCGCACAGTTCGATGAATCCAGAAAGCGCG 7294
4333 CATTTTCCACCATGATATTCGGCAAGCAGGATCGCATGGGTCAAGCAGAGTCTCGC 4392
7293 CATTTTCCACCATGATATTCGGCAAGCAGGATCGCATGGGTCAAGCAGAGTCTCGC 7234
4393 CGTCGGGATCGCGCGCTTGAAGCTTGGCAAGCTTGGCTGGCGCGAGCCCTGATGCT 4452
7233 CGTCGGGATCGCTCGCTTGAAGCTTGGCAAGCTTGGCTGGCGCGAGCCCTGATGCT 7174
4453 CTTCGTCCAGATCATCTGTATCGCAAGACCGGCTTCCATCCGAGTAGCTCGCTCGA 4512
7173 CTTCGTCCAGATCATCTGTATCGCAAGACCGGCTTCCATCCGAGTAGCTCGCTCGA 7114
4513 TGGATCTTTGGCTTGGTTCGNAATGGGAGGATAGCGGATCAAGCGTATGACGCGCC 4572
7113 TGGATCTTTGGCTTGGTTCGNAATGGGAGGATAGCGGATCAAGCGTATGACGCGCC 7054
4573 GCATTGATCAGCATGATGATGATCTTCGCGCAGGAGCAAGTGTAGATGACAGGAGAT 4632
7053 GCATTGATCAGCATGATGATGATCTTCGCGCAGGAGCAAGTGTAGATGACAGGAGAT 6994
4633 CTTCGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAAGTGAACAGTGA 4692
6993 CTTCGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAAGTGAACAGTGA 6934
4693 GCACAGTCCGCAAGGAAACCGCTTGTGGCCAGCCAGATAGCGCGCTGCTGCTGCT 4752
6933 GCACAGTCCGCAAGGAAACCGCTTGTGGCCAGCCAGATAGCGCGCTGCTGCTGCT 6874
4753 GCATTTTCAATTCAGGCGCACCGGACAGGTCGCTCTTGACAAAAAGAACCGGCGCCCTGG 4812
6873 GCATTTTCAATTCAGGCGCACCGGACAGGTCGCTCTTGACAAAAAGAACCGGCGCCCTGG 6814
4813 CTGACAGCGGAAACAGCGGGGATCAGAGCAGCGGATTTGTTGTGTGGCCAGTATAGC 4872
6813 CTGACAGCGGAAACAGCGGGGATCAGAGCAGCGGATTTGTTGTGTGGCCAGTATAGC 6754
4873 CGAATAGCTCTCCACCAAGCGCGGAGAACCTCGTGGCAATCATCTTGTTCATCA 4932
6753 CGAATAGCTCTCCACCAAGCGCGGAGAACCTCGTGGCAATCATCTTGTTCATCA 6694
4933 TCGCAACAGCTCTCATCTGCTCTTGTATGATGATCTTG 4971
6693 TCGCAACAGCTCTCATCTGCTCTTGTATGATGATCTTG 6655

Sequence 6, Application PC/TUS9610041		
GENERAL INFORMATION:		
APPLICANT:	White PhD, Kenneth	
APPLICANT:	Morrey PhD, John	
APPLICANT:	Reed, William	
TITLE OF INVENTION: Cassette for Expression of Lytic		
TITLE OF INVENTION: Peptides in Mammalian Transgenic Organisms		
NUMBER OF SEQUENCES: 32		
CORRESPONDENCE ADDRESS:		
ADDRESS: Trask Britt and Rossa		
STREET: P.O. Box 2550		
CITY: Salt Lake City		
STATE: Utah		
COUNTRY: USA		
ZIP: 84110		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Floppy disk		
COMPUTER: IBM PC compatible		
OPERATING SYSTEM: PC-DOS/MS-DOS		
SOFTWARE: Patent In Release #1.0, Version #1.30		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: PCT/US96/10041		
FILING DATE:		
CLASSIFICATION:		
ATTORNEY/AGENT INFORMATION:		
NAME: Sweigert PhD, Susan E		
REGISTRATION NUMBER: 36,289		
REFERENCE/DOCKET NUMBER: 2549		
TELECOMMUNICATION INFORMATION:		
TELEPHONE: 8015321922		
TELEFAX: 8015319168		
INFORMATION FOR SEQ ID NO: 6:		
SEQUENCE CHARACTERISTICS:		
LENGTH: 8797 base pairs		
TYPE: nucleic acid		
STRANDEDNESS: double		
TOPOLOGY: not relevant		
MOLECULE TYPE: other nucleic acid		
DESCRIPTION: /desc = "Construct comprising Bos		
DESCRIPTION: taurus beta casein 5' regulatory region plus genes encoding		
DESCRIPTION: amphipathic peptide and green fluorescent protein"		
HYPOTHETICAL: YES		
ANTI-SENSE: NO		
PCT-US96-10041-6		
Query Match	29.7%; Score 1569.8; DB 5; Length 8797;	
Best Local Similarity	86.3%; Pred. No. 0;	
Matches 1847; Conservative	0; Mismatches 112; Indels 180; Gaps 3;	
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Job time : 419 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 11:02:35 ; Search time 2155 Seconds
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12020.088 Million cell updates/sec

Title: US-09-921-143-36

Perfect score: 5283

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Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	1692.4	32.0	5225	15	US-10-286-186-16
C 5	1632.8	30.9	5285	14	US-10-038-001-1
6	1603.8	30.4	2192	15	US-10-021-403A-10
7	1603.8	30.4	3534	13	US-10-359-919A-11
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C 45	1569.8	29.7	4740	15	US-10-115-987B-13

ALIGNMENTS

RESULT 1

US-09-921-143-36
; Sequence 36, Application US/09921143
; Publication No. US20030215921A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Timothy
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PFI12P6
; CURRENT APPLICATION NUMBER: US/09/921,143
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/223,276
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 5283
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-921-143-36

Query Match	100.0%;	Score 5283;	DB 11;	Length 5283;
Best Local Similarity	100.0%;	Pred. No. 0;		
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QY 3481 GGTAACAGGATTTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGG 3540
 Db 3481 GGTAACAGGATTTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGG 3540
 QY 3541 CCTAACTACGGCTACACTAGAGAACAGTATTGTGTATCTGGCTCTGCTGAAGCCAGTT 3600
 Db 3541 CCTAACTACGGCTACACTAGAGAACAGTATTGTGTATCTGGCTCTGCTGAAGCCAGTT 3600
 QY 3601 ACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACCAACCCAGCTGGTAGCGT 3660
 Db 3601 ACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACCAACCCAGCTGGTAGCGT 3660
 QY 3661 GGTTTTTTTTGTTCGCAAGCAGAGTACGCGGCGAAGAAAGAGATCTCAGAAGATCCT 3720
 Db 3661 GGTTTTTTTTGTTCGCAAGCAGAGTACGCGGCGAAGAAAGAGATCTCAGAAGATCCT 3720
 QY 3721 TTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCAGCTTAAGGGATTTTG 3780
 Db 3721 TTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCAGCTTAAGGGATTTTG 3780
 QY 3781 GTCATGAGATTAATCGTGCACAAAGCGGCATCGTCTCCCACTCTCTGCAGTTTCGGG 3840
 Db 3781 GTCATGAGATTAATCGTGCACAAAGCGGCATCGTCTCCCACTCTCTGCAGTTTCGGG 3840
 QY 3841 GCATGGATGCGCGATAGCGCTGCTGTTTCTTGGATGCGCAGGATTTGCACTGCGG 3900
 Db 3841 GCATGGATGCGCGATAGCGCTGCTGTTTCTTGGATGCGCAGGATTTGCACTGCGG 3900
 QY 3901 TAGAACTCCCGAGGTGCTCCAGCTCAGGAGCAGCTGAACCAACTCAGGAGGGATTCG 3960
 Db 3901 TAGAACTCCCGAGGTGCTCCAGCTCAGGAGCAGCTGAACCAACTCAGGAGGGATTCG 3960
 QY 3961 AGCCCGGGTGGCGGAAGAACTCAGATGAGATCCCGCGCTGGAGGATCATCCAGCG 4020
 Db 3961 AGCCCGGGTGGCGGAAGAACTCAGATGAGATCCCGCGCTGGAGGATCATCCAGCG 4020
 QY 4021 GCCTCCCGGAAAAACGATTCGGAAGCCCAACTTTCATAGAGCGCGGTGGGAATCGAAA 4080
 Db 4021 GCCTCCCGGAAAAACGATTCGGAAGCCCAACTTTCATAGAGCGCGGTGGGAATCGAAA 4080
 QY 4081 TCTCGTGTAGGCAAGTTGGCGCTGCTGCTGCTCATTTGGAACCCAGAGTCCCGCTC 4140
 Db 4081 TCTCGTGTAGGCAAGTTGGCGCTGCTGCTGCTCATTTGGAACCCAGAGTCCCGCTC 4140
 QY 4141 AGAAGAACTCGTCAAGAGGCGATAGAGGCGATGCGCTGCGAATCGGAGCGCGATAC 4200
 Db 4141 AGAAGAACTCGTCAAGAGGCGATAGAGGCGATGCGCTGCGAATCGGAGCGCGATAC 4200
 QY 4201 CGTAAAGCAGGAGGAGCGGTGAGCCCATTCGCGCCAGAGCTTTTCAGCAATATCAGGG 4260
 Db 4201 CGTAAAGCAGGAGGAGCGGTGAGCCCATTCGCGCCAGAGCTTTTCAGCAATATCAGGG 4260
 QY 4261 TAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGCGCAGTGTGATATC 4320
 Db 4261 TAGCCAAACGCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGCGCAGTGTGATATC 4320
 QY 4321 CAGAAAAGGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATCGGTCACGA 4380
 Db 4321 CAGAAAAGGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATCGGTCACGA 4380
 QY 4381 CGAGATCTCGCGCTCGGGCATGCGGCTTGAAGCTGCGCAACAGTTCGGTGGCGGA 4440
 Db 4381 CGAGATCTCGCGCTCGGGCATGCGGCTTGAAGCTGCGCAACAGTTCGGTGGCGGA 4440
 QY 4441 GCGCTGTGCTCTTCTGCTCCAGATCATCTGATCGAAGACCGGCTTCCATCCAGTAC 4500
 Db 4441 GCGCTGTGCTCTTCTGCTCCAGATCATCTGATCGAAGACCGGCTTCCATCCAGTAC 4500
 QY 4501 GTGCTCGCTCGATCGGATGTTTCGTTGGTGGTGGAGGTGAGTGGCGGATCAAGCG 4560
 Db 4501 GTGCTCGCTCGATCGGATGTTTCGTTGGTGGTGGAGGTGAGTGGCGGATCAAGCG 4560
 QY 4561 TATGAGCGCGCGCATTTGCATCAGCCATGATGGATATCTTTCTCGGAGGAGCAAGGTGAG 4620

3666 TTTTGTCTTCAAGCAGCAGATTACCGCGCAGAGAAAAGGATCTCAAGAAGATCTTTTGAT 3725
Db |||||
5871 TTTTGTCTTCAAGCAGCAGATTACCGCGCAGAGAAAAGGATCTCAAGAAGATCTTTTGAT 6930
Qy CTTTCTACGGGCTCTGACGCTCAGTGGACGAAACTCAGCTTAAGGATTTTGTGAT 3785
Db |||||
6931 CTTTCTACGGGCTCTGACGCTCAGTGGACGAAACTCAGCTTAAGGATTTTGTGAT 6990
Qy 3786 GAGATTATCGTGCAGCAAAAGCGGCCATCGTGCTCTCCCACTCTCGCAGTTCGGGGCGATG 3845
Db |||||
6991 GAGATTATCAAAAAGGATCTTCACTAGATCTT----- 7024
Qy 3846 GATCGCGGATAGCCGCTCTGTTTCTTGGATCGGACGGAATTTGCACTGCGCGGTAGAA 3905
Db |||||
7025 ----- 7024
Qy 3906 CTCGCGAGGTGCTCCAGCCTCAGGCAGCAGCTGAACCACTCGCGAGGGGATCGAGCC 3965
Db |||||
7025 -----TT 7026
Qy 3966 GGGTGGCGAAGAACTCCAGATGAGATGCCGCTGGAGGATCATCCAGCCGCGTC 4025
Db |||||
7027 GGGTGGCGAAGAACTCCAGATGAGATGCCGCTGGAGGATCATCCAGCCGCGTC 7086
Qy 4026 CCGGAAAACGATTCCGAAGCCCAACTTTTCATAGAGCGCGGTGGAATCGAAATCTCG 4085
Db |||||
7087 CCGGAAAACGATTCCGAAGCCCAACTTTTCATAGAGCGCGGTGGAATCGAAATCTCG 7146
Qy 4086 TGATGGCAGGTTGGCGCTCGTGTGCTGATTCGAACCCAGAGTCCCGCTCAGAG 4145
Db |||||
7147 TGATGGCAGGTTGGCGCTCGTGTGCTGATTCGAACCCAGAGTCCCGCTCAGAG 7206
Qy 4146 AACTCGTCAAGAAGCGCATGAAGCGGATGCGTTCGAATCGGAGCGGCGATCCGTAA 4205
Db |||||
7207 AACTCGTCAAGAAGCGCATGAAGCGGATGCGTTCGAATCGGAGCGGCGATCCGTAA 7266
Qy 4206 AGCAGGAGGAAGCGCTCAGCCCATTCGCGCGCAGCTCTTCAGCAATATCAGCGGTAGCC 4265
Db |||||
7267 AGCAGGAGGAAGCGCTCAGCCCATTCGCGCGCAGCTCTTCAGCAATATCAGCGGTAGCC 7326
Qy 4266 AAGCTATGCTCTGATAGCGGTCCGCGCACACCCAGCGGCGACAGTGCATGATCCAGAA 4325
Db |||||
7327 AAGCTATGCTCTGATAGCGGTCCGCGCACACCCAGCGGCGACAGTGCATGATCCAGAA 7386
Qy 4326 AAGCGGCCATTTTCCACCATGATATTCGCAAGCAGCATCGCATGGGTCAAGCAGGA 4385
Db |||||
7387 AAGCGGCCATTTTCCACCATGATATTCGCAAGCAGCATCGCATGGGTCAAGCAGGA 7446
Qy 4386 TCCTCGCGCTCGGGCATGCGCGCTTGAGCTCGGCAAGCAGCATCGCATGGGTCAAGCAGGA 7446
Db |||||
7447 TCCTCGCGCTCGGGCATGCGCGCTTGAGCTCGGCAAGCAGCATCGCATGGGTCAAGCAGGA 7506
Qy 4446 TGATGCTCTTCTGCTCCAGATCATCTGATCGAAGACCGGCTTCCATCCGAGTACGTGCT 4505
Db |||||
7507 TGATGCTCTTCTGCTCCAGATCATCTGATCGAAGACCGGCTTCCATCCGAGTACGTGCT 7566
Qy 4506 CGCTCGATCGATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4565
Db |||||
7567 CGCTCGATCGATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7626
Qy 4566 AGCCGCGCATTCATCAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4625
Db |||||
7627 AGCCGCGCATTCATCAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7686
Qy 4626 AGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4685
Db |||||
7687 AGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7746
Qy 4686 ACGTTCGAGCAGCTGCGCAAGGAAAGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4745
Db |||||
7747 ACGTTCGAGCAGCTGCGCAAGGAAAGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7806

Qy 4746 TCGTCTCGAGTTCATTTCAGGCGACCGGACAGGTCTGCTTTCACAAAAGAACCGGCGC 4805
Db |||||
7807 TCGTCTCGAGTTCATTTCAGGCGACCGGACAGGTCTGCTTTCACAAAAGAACCGGCGC 7866
Qy 4806 CCCTGCGCTGACAGCGCGGAAACACCGCGGCATCAGAGCAGCGGATTCGTTGTGTGCGCCAG 4865
Db |||||
7867 CCCTGCGCTGACAGCGCGGAAACACCGCGGCATCAGAGCAGCGGATTCGTTGTGTGCGCCAG 7926
Qy 4866 TCATAGCGAATAGGCTCTTCCACCAAGCGCGGAGAACCTCGGTGCAATCCATCTTGT 4925
Db |||||
7927 TCATAGCGAATAGGCTCTTCCACCAAGCGCGGAGAACCTCGGTGCAATCCATCTTGT 7986
Qy 4926 TCAATCATGCGAAACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4985
Db |||||
7987 TCAATCATGCGAAACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8046
Qy 4986 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTGCAGGGCTTCCCAACCTTACCA 8046
Db |||||
8047 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTGCAGGGCTTCCCAACCTTACCA 8106
Qy 5046 GAGGCGCCCGCAGCTGGCAATTCGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5105
Db |||||
8107 GAGGCGCCCGCAGCTGGCAATTCGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 8166
Qy 5106 TATCGCCATGTAAGCCCACTGCAAGTACCTGCTTCTCTTTCGCGCTTTCGCTTTCGCTT 5165
Db |||||
8167 TATCGCCATGTAAGCCCACTGCAAGTACCTGCTTCTCTTTCGCGCTTTCGCTTTCGCTT 8226
Qy 5166 GTCAGATAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5225
Db |||||
8227 GTCAGATAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8286
Qy 5226 TTCTACGCTTCCGCTTCTTTCAGAGCCCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCG 5283
Db |||||
8287 TTCTACGCTTCCGCTTCTTTCAGAGCCCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCG 8344

RESULT 3
US-10-322-360-1/c
; Sequence 1, Application US/10322360
; Publication No. US20030165946A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: A Method for the Complete Chemical
; Synthesis and Assembly of Genes and Genomes
; FILE REFERENCE: P-EA 5511
; CURRENT APPLICATION NUMBER: US/10/322,360
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 09/554,929
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4800
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic plasmid
US-10-322-360-1

Query Match 33.9%; Score 1793.4; DB 15; Length 4800;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1;
Qy 3127 CATAGGCTCCGCCCCCTTCAGCAGCATCACAAAATCCAGCTCAAGTCAGAGGTGGCGA 3186
Db |||||
4800 CATAGGCTCCGCCCCCTTCAGCAGCATCACAAAATCCAGCTCAAGTCAGAGGTGGCGA 4741
Qy 3187 AACCCGACAGACTATAAGATACAGGCTTTCCTTGGAGCTCCCTCGTGGGCTCT 3246
Db |||||
4740 AACCCGACAGACTATAAGATACAGGCTTTCCTTGGAGCTCCCTCGTGGGCTCT 4681
Qy 3247 CCTGTTCCGACCTGCGCGCTTACCAGTACCTGTCGCGCTTCTCCCTTCGGGAAGCGTG 3306


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3926 ---TCAGGACAGCTGAACCACTCGCGAGGGATCGAGCCCGGGTGGGCGAAGAACT 3982
Db      |||||
4145 GGGTCACGTCGTCCTCCGACACACCGCGGAAGTCGTCCTCCACGAAGTCCCGGGAAC 4086
QY      |||||
3983 CAGCATGAGATCCCGCGCTGAGGATCATCCAGCCGCGCTCCCGGAAGAAAGATTCCGA 4042
Db      |||||
4085 CGAGCGGTGGTCCAGAACTCGACCGCTCCCGGACGTCGCGCGGTGAGCACCAGNA 4026
QY      |||||
4043 AGCCCAACCTTTCATAGAGAGGGCGGTGGAAATCGAAATCTCGTATGACGAGTTGGCG 4102
Db      |||||
4025 CGGCACTGGTCAACTGGCCATGGTCATGGTGGCCCTCTCACGTGCTATTATTGAAGCAATTATC 3966
QY      |||||
4103 TCGCTTGTGTCGGTCAATTCGAACCCCGAGAGTCCCG----- 4137
Db      |||||
3965 AGGGTTATGTCATGAGCGGATACATATTTGAATGATTTAGAAAAATAACAAATAG 3906
QY      |||||
4138 ----- 4137
Db      |||||
3905 GGGTTCGCGCACATTTCCCGGAAAGTGCCACCTGTATGCGGTGTGAATACGCCACAG 3846
QY      |||||
4138 -----CTCAGAGAACTC 4150
Db      |||||
3845 ATGCGTAGGAGAAAAATACCGCATCAGGAAATGTGAAGCGTTAATAATTGAGAAACTC 3786
QY      |||||
4151 GTCAGAGAGCGATAGAGGCGATGCGCTGCGAATCGGGAGCGGATACCGTAAAGCAC 4210
Db      |||||
3785 GTCAGAGAGCGATAGAGGCGATGCGCTGCGAATCGGGAGCGGATACCGTAAAGCAC 3726
QY      |||||
4211 GAGAAAGGTTACCCCATTCGCCGCCAAGCTCTTTCAGCAATATCACGGGTAGCCAAAGC 4270
Db      |||||
3725 GAGAAAGGTTACCCCATTCGCCGCCAAGCTCTTTCAGCAATATCACGGGTAGCCAAAGC 3666
QY      |||||
4271 TATGTCCTGATAGCGTCCGCCACACCGACCGGCGCCAGTCGATGAATCCAGAAAAAGC 4330
Db      |||||
3665 TATGTCCTGATAGCGTCCGCCACACCGACCGGCGCCAGTCGATGAATCCAGAAAAAGC 3606
QY      |||||
4331 GCCATTTCCACCATGATATTCGSCAAGCAGGATCGCCATGCTCGGCTGGCGGAGCCCTGATG 4450
Db      |||||
3605 GCCATTTCCACCATGATATTCGSCAAGCAGGATCGCCATGCTCGGCTGGCGGAGCCCTGATG 4390
QY      |||||
4391 GCGTGGGATGCGCGCTTGAGCCTTGGGAAAGCTTCGGCTGGCGGAGCCCTGATG 4450
Db      |||||
3545 GCGTGGGATGCTCGCTTGAGCCTTGGCGAAGCTTCGGCTGGCGGAGCCCTGATG 3486
QY      |||||
4451 CTCTCGTCAGATATCTGATCGACAGACCGGCTTCATCCGAGTACGTCGCTC 4510
Db      |||||
3485 CTCTCGTCAGATATCTGATCGACAGACCGGCTTCATCCGAGTACGTCGCTC 3426
QY      |||||
4511 GATCGATGTTTCGCTTGGTGGTTCGAATGGCAGGTAGCCGATCAAGCGTATGCGAGCGG 4570
Db      |||||
3425 GATCGATGTTTCGCTTGGTGGTTCGAATGGCAGGTAGCCGATCAAGCGTATGCGAGCGG 3366
QY      |||||
4571 CCGCATGTATCAGCATGATGGATATCTTCGCGAGGAGCAAGGTGAGTACAGAGGAG 4630
Db      |||||
3365 CCGCATGTATCAGCATGATGGATATCTTCGCGAGGAGCAAGGTGAGTACAGAGGAG 3306
QY      |||||
4631 ATCTCCCGCGGACATTCGCCAATAGCAGCAGTCCCTTCGCGCTTCAGTACAAAGCTC 4690
Db      |||||
3305 ATCTCCCGCGGACATTCGCCAATAGCAGCAGTCCCTTCGCGCTTCAGTACAAAGCTC 3246
QY      |||||
4691 GAGCAGCTGCGCAAGGAAGCCCGCTGTCGCGAGCCAGTACGCGGCTGCTCGTC 4750
Db      |||||
3245 GAGCAGCTGCGCAAGGAAGCCCGCTGTCGCGAGCCAGTACGCGGCTGCTCGTC 3186
QY      |||||
4751 CTGCAAGTTCAATCAGGCAACCGGACAGGTGCGTCTTGACAAAAAGAACCGGGCGCCCTG 4810
Db      |||||
3185 TTGCAAGTTCAATCAGGCAACCGGACAGGTGCGTCTTGACAAAAAGAACCGGGCGCCCTG 3126
QY      |||||
4811 CGCTGACGCGGAAACACCGCGGATCAGAGAGCGGATGTCGTGTCGCCAGTCATA 4870
Db      |||||
3125 CGCTGACGCGGAAACACCGCGGATCAGAGAGCGGATGTCGTGTCGCCAGTCATA 3066
QY      |||||
4871 GCCGAATAGCCTCTCCACCCAAAGCGCGGAGAACCTGCGTGAATTCATCTTTGTTCAAT 4930
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Db      |||||
3065 GCCGAATAGCTCTCCACCAGAGCGCCGGAGAACTGCGTGAATCCATCTTTGTTCAAT 3006
QY      |||||
4931 CATGGAACGATCTCTCATCTCTGTCTTTGATCAGATCTTGTATCCCTCGGCATCAGAT 4990
Db      |||||
3095 CATGGAACGATCTCTCATCTCTGTCTTTGATCAGAGCTTGTATCCCTCGGCATCAGAT 2946
QY      |||||
4991 CTTGCGGCGAAGAAAGCATCCAGTTTACTTTTTCAGGGCTTCCCAACCTTACAGAGG 5050
Db      |||||
2945 CTTGCGGCGGAGAAAGCATCCAGTTTACTTTTTCAGGGCTTCCCAACCTTACAGAGG 2886
QY      |||||
5051 CGCCCAAGCTGCGCAATTCGGGTTCCGTTTCTGTTGTCATAAACCGCCAGCTTAGCTATCG 5110
Db      |||||
2885 CGCCCAAGCTGCGCAATTCGGGTTCCGTTTCTGTTGTCATAAACCGCCAGCTTAGCTATCG 2826
QY      |||||
5111 CCATGTAAAGCCACTGCAAGCTACTGCTTTCTTTTTCGCTTGGCTTTCCCTTGTCCA 5170
Db      |||||
2825 CCATGTAAAGCCACTGCAAGCTACTGCTTTCTTTTTCGCTTGGCTTTCCCTTGTCCA 2766
QY      |||||
5171 GATAGCCAGTAGCTGACATTCATCCCGGGTCAGACCGTTTCTGCGACTGGCTTTCTA 5230
Db      |||||
2765 GATAGCCAGTAGCTGACATTCATCCCGGGTCAGACCGTTTCTGCGACTGGCTTTCTA 2706
QY      |||||
5231 CGTG 5234
Db      |||||
2705 CGTG 2702
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RESULT 6

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US-10-021-403A-10
; Sequence 10, Application US/10021403A
; Publication No. US20030074679A1
; GENERAL INFORMATION:
; APPLICANT: Advisis
; TITLE OF INVENTION: Administration of Nucleic Acid Sequence to Female Animal to Enhanc
; FILE OF INVENTION: Growth in Offspring
; FILE REFERENCE: HO-P0201US/100021476/OTA 00-91
; CURRENT APPLICATION NUMBER: US/10/021,403A
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/255,021
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 2192
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: This is a plasmid vector comprising a pVC0289 backbone
US-10-021-403A-10
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Query Match 30.4%; Score 1603.8; DB 15; Length 2192;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

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QY      2706 CTAGAGTAATCATGTCATAGCTGTTCTCTGTGGAATTTGTTATCCGCTCACAATTC 2765
Db      70 CTGGGTAAATCATGTCATAGCTGTTCTCTGTGGAATTTGTTATCCGCTCACAATTC 129
QY      2766 ACACACATACGAGCGGAGCATAAAGTAAAGCTCGGGTGCCTAATGATGAGCTA 2825
Db      130 ACACACATACGAGCGGAGCATAAAGTAAAGCTCGGGTGCCTAATGATGAGCTA 189
QY      2826 ACTCAATTAATTTGGTTCGCTCACTGCCGCTTTTCCAGTCGGGAAACCTTCGTCGCA 2885
Db      190 ACTCAATTAATTTGGTTCGCTCACTGCCGCTTTTCCAGTCGGGAAACCTTCGTCGCA 249
QY      2886 GGTGCAATTAATTAATTCGCGCAACCGCGGAGAGCGGTTTGGTATTTGGCGCTCTTC 2945
Db      250 GGTGCAATTAATTAATTCGCGCAACCGCGGAGAGCGGTTTGGTATTTGGCGCTCTTC 309
QY      2946 CGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3005
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RESULT 7
 US-10-359-919A-11
 ; Sequence 11, Application US/10359919A
 ; Publication No. US20040038918A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baylor College of Medicine
 ; TITLE OF INVENTION: Modified Pituitary Gland Development in offspring from Explant
 ; TITLE OF INVENTION: animals treated with GHRH
 ; FILE REFERENCE: 109328.00087 - AVSI-0019
 ; CURRENT APPLICATION NUMBER: US/10/359,919A
 ; CURRENT FILING DATE: 2003-02-06
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 3534
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Nucleic acid sequence of the HV-GHRH plasmid.
 US-10-359-919A-11

Query Match 30.4%; Score 1603.8; DB 13; Length 3534;
 Best Local Similarity 82.8%; Pred. No. 0;
 Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;
 QY 2706 CTAGACGTAATCATGTCATAGCTGTTCTCTGTGTGAATTTGTTATCGCGTCAAAATTC 2765
 DB 1412 CTTGGCGTAATCATGTCATAGCTGTTCTCTGTGTGAATTTGTTATCGCGTCAAAATTC 1471
 QY 2766 ACACAAATACGAGCCGGAAGCAATAAGTGTAAAGCCCTGGGGTCCCTAATGAGTACGTA 2825
 DB 1472 ACACAAATACGAGCCGGAAGCAATAAGTGTAAAGCCCTGGGGTCCCTAATGAGTACGTA 1531
 QY 2826 ACTCACATTAATTCGTTGCGTCACTGCCGCTTTCAGTCGGGAAACCTGTCGCCA 2885
 DB 1532 ACTCACATTAATTCGTTGCGTCACTGCCGCTTTCAGTCGGGAAACCTGTCGCCA 1591
 QY 2886 GCTGCATTAATGAATCGGCCAAACGCGGGGAGAGCGGTTTGGTATTGGCGCTCTTC 2945
 DB 1592 GCTGCATTAATGAATCGGCCAAACGCGGGGAGAGCGGTTTGGTATTGGCGCTCTTC 1651
 QY 2946 CGCTTCTCGCTCACTGACTCGCTGCGCTGCGTCTGCGTCTGCGGCGAGCGGTATCAGC 3005
 DB 1652 CGCTTCTCGCTCACTGACTCGCTGCGTCTGCGTCTGCGGCGAGCGGTATCAGC 1711
 QY 3006 TCACTCAAGCGCGTAAATACGGTTATCCACAGAAATCAGGGGATAACGACGAAAGAACAT 3065
 DB 1712 TCACTCAAGCGCGTAAATACGGTTATCCACAGAAATCAGGGGATAACGACGAAAGAACAT 1771
 QY 3066 GTGACGAAAGGCGCAGCAAGGCGAGGACCGTAAAGGCGCGTGTGTCGCGTTTTT 3125
 DB 1772 GTGACGAAAGGCGCAGCAAGGCGAGGACCGTAAAGGCGCGTGTGTCGCGTTTTT 1831
 QY 3126 CCATAGGCTCCGCGCCCTGACGAGCATCACAAATATCAGCGTCAAGTCAAGTCAGAGTGGG 3185
 DB 1832 CCATAGGCTCCGCGCCCTGACGAGCATCACAAATATCAGCGTCAAGTCAAGTCAGAGTGGG 1891
 QY 3186 AAACCCGACGAGCTATAAGATACAGCGGTTTCCCGCTGGAAGTCCCTCTGTCGCTC 3245
 DB 1892 AAACCCGACGAGCTATAAGATACAGCGGTTTCCCGCTGGAAGTCCCTCTGTCGCTC 1951
 QY 3246 TCCGTTCGACCGCTGCGCTTACCGGATACCTGTCCGCTTTCCTTCGCGAAGCGT 3305
 DB 1952 TCCGTTCGACCGCTGCGCTTACCGGATACCTGTCCGCTTTCCTTCGCGAAGCGT 2011
 QY 3306 GCGGCTTTCTCATAGCTCAGCTGTAGTATCTCAGTTCGGTGTAGTCTGCTCCAA 3365
 DB 2012 GCGGCTTTCTCATAGCTCAGCTGTAGTATCTCAGTTCGGTGTAGTCTGCTCCAA 2071
 QY 3366 GCTGGGCTGTGTGACGAAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAACTA 3425
 DB 2072 GCTGGGCTGTGTGACGAAACCCCGCTTCAGCCGACCGCTGCGCTTATCCGGTAACTA 2131

QY 3426 TCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCAGCTGTAA 3485
 DB 2132 TCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCAGCTGTAA 2191
 QY 3486 CAGGATTAGCAGAGCGAGGTATGTAGGGTCTACAGAGTCTTGAAGTGGTGGCTAA 3545
 DB 2192 CAGGATTAGCAGAGCGAGGTATGTAGGGTCTACAGAGTCTTGAAGTGGTGGCTAA 2251
 QY 3546 CTACGGCTACACTAGAGAAACAGTATTTGGTATCTGCGTCTGCTGAAGCCAGTTACCTT 3605
 DB 2252 CTACGGCTACACTAGAGAAACAGTATTTGGTATCTGCGTCTGCTGAAGCCAGTTACCTT 2311
 QY 3606 CGGAAAAGAGTTGCTAGCTCTTGTATCCGGGAAACAAACCCAGCTGTGTGGTGGTT 3665
 DB 2312 CGGAAAAGAGTTGCTAGCTCTTGTATCCGGGAAACAAACCCAGCTGTGTGGTGGTT 2371
 QY 3666 TTTTGTTCGAAAGCAGCAGATTAACGCGCAGAAAAAGGATCTCAAGAGATCTCTTTGAT 3725
 DB 2372 TTTTGTTCGAAAGCAGCAGATTAACGCGCAGAAAAAGGATCTCAAGAGATCTCTTTGAT 2431
 QY 3726 CTTTCTACGGGGTCTGACGCTCAGTGGAAACAAACTCAGCTTAAGGATTTTGGTCAAT 3785
 DB 2432 CTTTCTACGGGGTCTGA----- 2449
 QY 3786 GAGATTATCGTCGACCAAGCGGCCATGTCCTCCCACTCTCTGAGTTCCGGGGCATG 3845
 DB 2450 ----- 2449
 QY 3846 GATGCGCGATAGCGCTGCTGTTCTTGTATCCGACGATTTGCACTGCCCGGTAGAA 3905
 DB 2450 ----- 2449
 QY 3906 CTCGCGAGTCTGTCAGCTCAGCCTCAGCAGCAGTGAACCACTCGCAGGGGATCGAGCC 3965
 DB 2450 ----- 2449
 QY 3966 GGGGTGGCGAAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGGCGTC 4025
 DB 2450 ----- 2449
 QY 4026 CCGGAAAAAGTATCCGAAAGCCCAACTTTTATAGAGAGCGCGGTGGAATCGAAATCTCG 4085
 DB 2450 ----- 2449
 QY 4086 TGATGCGAGTTGGGCGTCTGTTGGTCTGTTTTCATAGAGAGCGCGGTGGAATCGAAATCTCG 4145
 DB 2450 -----CGCTCAGAG 2459
 QY 4146 AACTCGTCAAGAGCGATAGAGCGGATGCGCTGCGATCGGAGCGGCGATACCGTAA 4205
 DB 2460 AACTCGTCAAGAGCGGATAGAGCGGATGCGCTGCGAATCGGAGCGGCGATACCGTAA 2519
 QY 4206 AGCAGAGAGAGCGGTGAGCGGATTCGCGCCAAAGCTCTTCAAGATATCAAGGTAGCC 4265
 DB 2520 AGCAGAGAGAGCGGTGAGCGGATTCGCGCCAAAGCTCTTCAAGATATCAAGGTAGCC 2579
 QY 4266 AACGCTATGCTCTGATAGCGGTCGCCCAACCCAGCGGCGCAGTCAATGAATCAGAA 4325
 DB 2580 AACGCTATGCTCTGATAGCGGTCGCCCAACCCAGCGGCGCAGTCAATGAATCAGAA 2639
 QY 4326 AAGCGGCAATTTCCACCATGATATTCGCAAGAGGAGGATCGCCATGGTCAAGCAGAA 4385
 DB 2640 AAGCGGCAATTTCCACCATGATATTCGCAAGAGGAGGATCGCCATGGTCAAGCAGAA 2699
 QY 4386 TCCTCGCGTGGGCGATGCGGCTTGTAGCTGCGGAAAGTTCGGTGGCGGCGGCGCC 4445
 DB 2700 TCCTCGCGTGGGCGATGCGGCTTGTAGCTGCGGAAAGTTCGGTGGCGGCGGCGCC 2759
 QY 4446 TGATGCTCTTCTGTCAGATCATCTCTGATCGAAGACCGGCTTCCATCCGAGTACGTCT 4505
 DB 2760 TGATGCTCTTCTGTCAGATCATCTCTGATCGAAGACCGGCTTCCATCCGAGTACGTCT 2819

Thu Aug 5 08:55:54 2004

4506	QY	CGCTCGAATGCGATGTTTCCTTGTGTGCTCGAATGGCGAGTATAGCCGGATCAAGCGTATGC	4565
2820	Db	CGCTCGAATGCGATGTTTCCTTGTGTGCTCGAATGGCGAGTATAGCCGGATCAAGCGTATGC	2879
4566	QY	AGCCGCGCATTCGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC	4625
2880	Db	AGCCGCGCATTCGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGAC	2939
4626	QY	AGGAGATCCTTCGCCCCCGGCACCTTCGCCCAATAGACAGCCAGTCCCTTCCCGCTTCAGTGACA	4685
2940	Db	AGGAGATCCTTCGCCCCCGGCACCTTCGCCCAATAGACAGCCAGTCCCTTCCCGCTTCAGTGACA	2999
4686	QY	ACGTGCGACACAGCTGCGGCAAGGAACGCCCGTCTGTGCCAGCACGATAGCCGCGCTGCC	4745
3000	Db	ACGTGCGACACAGCTGCGGCAAGGAACGCCCGTCTGTGCCAGCACGATAGCCGCGCTGCC	3059
4746	QY	TCGTCTCTCGAGTTCATTTCAGGGCACCCGACAGGTTCGGTCTTTGACAAAAAGAACCGGGCGC	4805
3060	Db	TCGTCTCTCGAGTTCATTTCAGGGCACCCGACAGGTTCGGTCTTTGACAAAAAGAACCGGGCGC	3119
4806	QY	CCCTGGCGTGACACGCCGGACACACGGCGGATCAGACAGCCGATTCCTGTGTTGTCGCCAG	4865
3120	Db	CCCTGGCGTGACACGCCGGACACACGGCGGATCAGACAGCCGATTCCTGTGTTGTCGCCAG	3179
4866	QY	TCATAGCCGATAGCTCTCCACCAAGCGCGCGAGAACCTCGTGCATCCATCTTGT	4925
3180	Db	TCATAGCCGATAGCTCTCCACCAAGCGCGCGAGAACCTCGTGCATCCATCTTGT	3239
4926	QY	TCAATCATCGAAACGATCCTCATCTGCTCTCTTGATCAGATCTTGATCCCTGCGCCAT	4985
3240	Db	TCAATCATCGAAACGATCCTCATCTGCTCTCTTGATCAGATCTTGATCCCTGCGCCAT	3299
4986	QY	CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGAGGGCTTCCCAAACCTTACCA	5045
3300	Db	CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGAGGGCTTCCCAAACCTTACCA	3359
5046	QY	GAGGGCGCCACAGCTGGCAATTCGGGTTTCGCTGCTGTGCCATAAAACCGGCCAGTCTAGC	5105
3360	Db	GAGGGCGCCACAGCTGGCAATTCGGGTTTCGCTGCTGTGCCATAAAACCGGCCAGTCTAGC	3419
5106	QY	TATCGCCATGTAAAGCCCATCGCAAGCTACCTGCTTCTCTT	5146
3420	Db	AACCTGTGTGAAGGGCGATTCGGTGGCGGCTCTTCGCTATT	3460

[illegible]

3846 GATGCGGATAGCCGCTGCTGGTTCTCTGGATGCGGACGGATTTCGACTGCGCGTAGAA 3905
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3906 CTCGCGAGGTGTCACAGCCTCAGGACGAGCTGAACCACTCGCGAGGGATCGAGCC 3965
2450 ----- 2449
3966 GGGGTGGCGAAGAACTCCAGATGAGATCCCGCGCTGGAGGATCATCCAGCGCGCTC 4025
2450 ----- 2449
4026 CCGGAAACGATTCCGAAGCCCAACCTTTCATAGAGGCGGGGTGGAATCGAAATCTCG 4085
2450 ----- 2449
4086 TGATGGCAGTTGGGCGTCTGCTTGGTGGTCAATTTGGAACCCAGAGTCCCGCTCAGAAG 4145
2450 ----- 2449
4146 AACTCGTCAAGAGCGGATGAGAGCGATGCGTGGGAATCGGAGCGCGATACCGTAA 4205
2460 AACTCGTCAAGAGCGGATGAGAGCGATGCGTGGGAATCGGAGCGCGATACCGTAA 2519
4206 AGCAGGAGGAGCGGTGAGCCATTGCGCGCAAGCTCTTCAGCAATATCAGGGGTAGCC 4265
2520 AGCAGGAGGAGCGGTGAGCCATTGCGCGCAAGCTCTTCAGCAATATCAGGGGTAGCC 2579
4266 AAGCTATGCTGATAGCGGTCCGCACACCCAGCGCGCACAGTCCGATGAATCCAGAA 4325
2580 AAGCTATGCTGATAGCGGTCCGCACACCCAGCGCGCACAGTCCGATGAATCCAGAA 2639
4326 AAGCGGCATTTCCACCATGATATTCGGAGAGCGGATCGCCATCGGTACAGACGAGA 4385
2640 AAGCGGCATTTCCACCATGATATTCGGAGAGCGGATCGCCATCGGTACAGACGAGA 2699
4386 TCCTCGCGCTCGGCGATCGCGCTTCAGCTTCGCGAACAGTTCGGTGGGCGGAGCCCC 4445
2700 TCCTCGCGCTCGGCGATCGCGCTTCAGCTTCGCGAACAGTTCGGTGGGCGGAGCCCC 2759
4446 TGATGCTCTTTCGTCAGATCATCTGATCGACAAAGACCGGCTTCATCCGAGTACGTC 4505
2760 TGATGCTCTTTCGTCAGATCATCTGATCGACAAAGACCGGCTTCATCCGAGTACGTC 2819
4506 CGCTCGATGCGATGTTTCGCTTGGTGGTGAATGGGAGGTAGCCGATCAAGCGTATGC 4565
2820 CGCTCGATGCGATGTTTCGCTTGGTGGTGAATGGGAGGTAGCCGATCAAGCGTATGC 2879
4566 AGCGCGCGATTCATCGATCAGCATGATGATACCTTCGCGAACAGTTCGGTGGGCGGAGCCCC 4625
2880 AGCGCGCGATTCATCGATCAGCATGATGATACCTTCGCGAACAGTTCGGTGGGCGGAGCCCC 2939
4626 AGGAGTCTGCGCGGCACTTCGCGCAATAGCAGCAGTTCCTTCGCGTTCAGTGACA 4685
2940 AGGAGTCTGCGCGGCACTTCGCGCAATAGCAGCAGTTCCTTCGCGTTCAGTGACA 2999
4686 AGCTGAGCAGAGCTCGCAAGAAAGCCCGTGGTGGGAGCAACGATAGCGCGTGC 4745
3000 AGCTGAGCAGAGCTCGCAAGAAAGCCCGTGGTGGGAGCAACGATAGCGCGTGC 3059
4746 TCGTCTGAGTTCATTTCAGGCGACCGGACAGTTCGCTTCGCAAAAGAACCGGGCGC 4805
3060 TCGTCTGAGTTCATTTCAGGCGACCGGACAGTTCGCTTCGCAAAAGAACCGGGCGC 3119
4806 CCGTGGCTGACAGCGGGAACAGCGGCGATCAGAGCAGCCGATTCGTTGTCGCCAG 4865
3120 CCGTGGCTGACAGCGGGAACAGCGGCGATCAGAGCAGCCGATTCGTTGTCGCCAG 3179
4866 TCATAGCCGAATAGCTCTCCACCCAGCGGCGAGAACCTTCGTCGAATCATCTTGT 4925
3180 TCATAGCCGAATAGCTCTCCACCCAGCGGCGAGAACCTTCGTCGAATCATCTTGT 3239
4926 TCAATCATGCGAAACGATCTCTCATCTGCTCTTGTATCAGATCTTGATCCCTCGCGCAT 4985

3240 TCAATCATGCGAAACGATCTCTCTCTCTGATCAGATCTTGATCCCTCGGCCAT 3299
4986 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTACTTTGCAGGGCTTCCCAACCTTACCA 5045
3300 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTACTTTGCAGGGCTTCCCAACCTTACCA 3359
5046 GAGGCGCGCCAGCTGGCAATTCGGTTTCGTTGCTGTCATATAAAGCCGCGAGTACG 5105
3360 GAGGCGCGCCAGCTGGCAATTCGGTTTCGTTGCTGTCATATAAAGCCGCGAGTACG 3419
5106 TATCGCCATGTAAGCCCACTCAAGCTACCTGCTTCTCTT 5146
3420 AACTGTTGGGAGGCGGATCGTGGGCGCTCTTCGCTATT 3460

RESULT 9

US-10-359-919A-13
; Sequence 13, Application US/10359919A
; Publication No. US20040038918A1
; GENERAL INFORMATION:
; APPLICANT: Baylor College of Medicine
; TITLE OF INVENTION: Modified Pituitary Gland Development in offspring from Expectant
; FILE REFERENCE: 108328.00087 - AVSI-0019
; CURRENT APPLICATION NUMBER: US/10/359,919A
; CURRENT FILING DATE: 2003-02-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Nucleic acid sequence of the TV-GHRH plasmid.
US-10-359-919A-13

Query Match 30.4%; Score 1603.8; DB 13; Length 3534;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;
3240 2706 CTAGACGTAATCATGCTCATAGCTGTTCTCTGTTGTAATTTATCCGCTCACAATTC 2765
1412 CTGCGGTAATCATGCTCATAGCTGTTCTCTGTAATTTATCCGCTCACAATTC 1471
2766 ACACACATACGAGCGGAGCATAAAGTAAAGCTGGGTCCTAATGAGTGAGCTA 2825
1472 ACACACATACGAGCGGAGCATAAAGTAAAGCTGGGTCCTAATGAGTGAGCTA 1531
2826 ACTCACATTAATTGCGTTGCGTCACTGCGGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
1532 ACTCACATTAATTGCGTTGCGTCACTGCGGCTTTCCAGTCGGGAAACCTGTCGTGCCA 1591
2886 GTGCAATTAATGAATCGGCAACCGCGGGGAGAGCGGTTTTCGTTATTTGGGCGCTTTC 2945
1592 GCTGCATTAATGAATCGGCAACCGCGGGGAGAGCGGTTTTCGTTATTTGGGCGCTTTC 1651
2946 CGCTTCTCTGCTCACTGATCTCGCTGCGTTCGCTTCGCTTCGCGGAGCGGTATCAGC 3005
1652 CGCTTCTCTGCTCACTGATCTCGCTGCGTTCGCTTCGCTTCGCGGAGCGGTATCAGC 1711
3006 TCACCTCAAGAGGGGTAATACGGTTATCCACAGAAATCAGGGGATACGCGAGGAAACAT 3065
1712 TCACCTCAAGAGGGGTAATACGGTTATCCAGAAATCAGGGGATACGCGAGGAAACAT 1771
3066 GTGACAAAAGGCCAGCAAAAGCCAGGAAACCGTAAAAAGGCGGTTTCTGCGCTTTT 3125
1772 GTGACAAAAGGCCAGCAAAAGCCAGGAAACCGTAAAAAGGCGGTTTCTGCGCTTTT 1831
3126 CCATAGGCTTCGCGCCCTTGAGAGCATCAAAAAATCGAGCTCAAGTCAAGGTGGCG 3185
1832 CCATAGGCTTCGCGCCCTTGAGAGCATCAAAAAATCGAGCTCAAGTCAAGGTGGCG 1891

QY	3186	AAACCCGACGAGTAAATAAAGATACCAAGCGGCTTTCCCTCGAAAGCTCCCTCGTGGCGTC	3245	Db	2580	AAACCTATGCTCTGATAGCGTCCGCGACACCCAGCGCGGCACAGTCGATGAATCCAGAA	2639
Db	1892	AAACCCGACGAGTAAATAAAGATACCAAGCGGCTTTCCCTCGAAAGCTCCCTCGTGGCGTC	1951	QY	4326	AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCCACGACGAGA	4385
QY	3246	TCCTGTTCCGACCGCTCGCGCTTACCGGATACCTGTCGCGCTTTCCCTCGGGAAGCGT	3305	Db	2640	AAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCCACGACGAGA	2699
Db	1952	TCCTGTTCCGACCGCTCGCGCTTACCGGATACCTGTCGCGCTTTCCCTCGGGAAGCGT	2011	QY	4386	TCCTCGCGCTCGGCGCATCGCGCGCTTGAAGCTTGGCGAAACAGTTCCGCTGGCGCGAGCC	4445
QY	3306	GGCGCTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTCCGCTGAGGTGCTTCGCTCCAA	3365	Db	2700	TCCTCGCGCTCGGCGCATCGCGCGCTTGAAGCTTGGCGAAACAGTTCCGCTGGCGCGAGCC	2759
Db	2012	GGCGCTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTCCGCTGAGGTGCTTCGCTCCAA	2071	QY	4446	TGATGCTCTTCCGTCAGATCATCTGATCGAACAAGACCGGCTTCCATCCGAGTACGTCT	4505
QY	3366	GCTGGCTGTGTGACGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCGCTAACCTA	3425	Db	2760	TGATGCTCTTCCGTCAGATCATCTGATCGAACAAGACCGGCTTCCATCCGAGTACGTCT	2819
Db	2072	GCTGGCTGTGTGACGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCGCTAACCTA	2131	QY	4506	CGCTCGATGCGATGTTTCCGCTTGGTGGTTCGAATGGCAGGATAGCGGATCAAGCGTATGC	4565
QY	3426	TGCTTTGAGTCCAAACCGGTTAAGACACGACTTATCGCCACTGGCAGGACCACTGGTAA	3485	Db	2820	CGCTCGATGCGATGTTTCCGCTTGGTGGTTCGAATGGCAGGATAGCGGATCAAGCGTATGC	2879
Db	2132	TGCTTTGAGTCCAAACCGGTTAAGACACGACTTATCGCCACTGGCAGGACCACTGGTAA	2191	QY	4566	AGCGCGCCGATTCGATCAGCCATGATGATATCTTCTCGGCAAGGAGCAAGGTGAGTAC	4625
QY	3486	CAGGATAGCAGGAGGTATGTAGGCGGTGCTACAGAGTTCCTTGAAGTGGTGGCTTAA	3545	Db	2880	AGCGCGCCGATTCGATCAGCCATGATGATATCTTCTCGGCAAGGAGCAAGGTGAGTAC	2939
Db	2192	CAGGATAGCAGGAGGTATGTAGGCGGTGCTACAGAGTTCCTTGAAGTGGTGGCTTAA	2251	QY	4626	AGGAGATCCTGCCCCCGGCACTTCGCGCCAAATAGCAGCCATGCTTCCCGCTTCAGTGACA	4685
QY	3546	CTACGCTACACTAGAAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT	3605	Db	2940	AGGAGATCCTGCCCCCGGCACTTCGCGCCAAATAGCAGCCATGCTTCCCGCTTCAGTGACA	2999
Db	2252	CTACGCTACACTAGAAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT	2311	QY	4686	AGCTCGAGCAGACTGCGCAAGCAAGCGCCGCTGCTGGCCAGGACCAAGATACCGCGCTGCC	4745
QY	3606	CGGAAAGAGTTGGTAGCTCTTGATCGGCAACCAACACCGCTGCTGAGCGTGGTTT	3665	Db	3000	AGCTCGAGCAGACTGCGCAAGCAAGCGCCGCTGCTGGCCAGGACCAAGATACCGCGCTGCC	3059
Db	2312	CGGAAAGAGTTGGTAGCTCTTGATCGGCAACCAACACCGCTGCTGAGCGTGGTTT	2371	QY	4746	TGCTCTGCTGAGTTCATTACAGGCGCACCGGACAGGTCTGTTGACAAAAAGACCGGCGCG	4805
QY	3666	TTTGTGTTCAAGCAGCAGTACCGCGCAGAAAAAAGGATCTCAAGAAAGATCCTTTGAT	3725	Db	3060	TGCTCTGCTGAGTTCATTACAGGCGCACCGGACAGGTCTGTTGACAAAAAGACCGGCGCG	3119
Db	2372	TTTGTGTTCAAGCAGCAGTACCGCGCAGAAAAAAGGATCTCAAGAAAGATCCTTTGAT	2431	QY	4806	CCCTGCTGCTGACAGCGGCAACACCGCGGATCAGAGCGGCGATCTGCTGCTGCGCCAG	4865
QY	3726	CTTTTCTACGGGCTGTCAGCTCAGTGGAAACGAAACTCAGTGAAGGATTTTGGTCAT	3785	Db	3120	CCCTGCTGCTGACAGCGGCAACACCGCGGATCAGAGCGGCGATCTGCTGCTGCGCCAG	3179
Db	2432	CTTTTCTACGGGCTGTCAGTGGAAACGAAACTCAGTGAAGGATTTTGGTCAT	2449	QY	4866	TCATAGCCGATAGCTCTCCACCAAGCGGCGCGGAGAACCTCGTGCAATCCATCTTGT	4925
QY	3786	GAGATATGTCGACAAAGCGGCCATCGTGGCTCCCACTCCCTGCGAGTTCCGGGGCATG	3845	Db	3180	TCATAGCCGATAGCTCTCCACCAAGCGGCGCGGAGAACCTCGTGCAATCCATCTTGT	3239
Db	2450	-----	2449	QY	4926	TCATCATGCGAAACGATCCTCATCTCTCTCTGATCAGATCTTGATCCCTGCGGCAT	4985
QY	3846	GATGCGGATAGCGCGTCTGCTGTTTCTTGATGCGAGCGGATTTGCACTGCGGATGAA	3905	Db	3240	TCATCATGCGAAACGATCCTCATCTCTCTCTGATCAGATCTTGATCCCTGCGGCAT	3299
Db	2450	-----	2449	QY	4986	CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGAGGCGCTTCCCAACCTTACCA	5045
QY	3906	CTCCGCGAGTCTGTCAGCTCAGGCGCAGCTGAACCAACTCCGAGGGGATCGAGCCC	3965	Db	3300	CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGAGGCGCTTCCCAACCTTACCA	3359
Db	2450	-----	2449	QY	5046	GAGGCGCCCGCAGCTGCGCAATTCGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5105
QY	3966	GGGTGGGCGAAGNACTCCAGATGAGATCCCGCGCTGGAGGATCATCCAGCGCGGCTC	4025	Db	3360	GAGGCGCCCGCAGCTGCGCAATTCGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3419
Db	2450	-----	2449	QY	5106	TATCGCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTT	5146
QY	4026	CCGAAACGATTCGAAAGCCCAACTTTTCATAGAGCGCGGCTGGAAATCGAATCTCG	4085	Db	3420	AACCTGTTGGGAAGGCGATCGGTGCGGCGCTCTTTCGCTATT	3460
Db	2450	-----	2449	RESULT 10			
QY	4086	TGATGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	4145	US-10-359-919A-14			
Db	2450	-----	2459	; Sequence 14, Application US/10359919A			
QY	4146	AACCTGTCAGAAAGCGATAGAGCGATGCGTTCGCAATCGGAGCGGCGATACCGTAA	4205	; Publication No. US20040038918A1			
Db	2460	AACCTGTCAGAAAGCGATAGAGCGATGCGTTCGCAATCGGAGCGGCGATACCGTAA	2519	; GENERAL INFORMATION:			
QY	4206	AGCAGGAGGAGCGGTACGCCATTCGCGCGCAAGCTCTTACGCAATATCAGGTAACC	4265	; APPLICANT: Baylor College of Medicine			
Db	2520	AGCAGGAGGAGCGGTACGCCATTCGCGCGCAAGCTCTTACGCAATATCAGGTAACC	2579	; TITLE OF INVENTION: Modified Pituitary Gland Development in offspring from Expectant			
QY	4266	AACGCTATGCTGATAGGCTCCGCGCACCCAGCGCGCCACAGTCGATGAATCCAGAA	4325	; FILE REFERENCE: 108328.00087 - AVSI-0019			
				; CURRENT APPLICATION NUMBER: US/10/359,919A			
				; CURRENT FILING DATE: 2003-02-06			
				; NUMBER OF SEQ ID NOS: 15			
				; SOFTWARE: Patent version 3.1			

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; SEQ ID NO 14
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Nucleic acid sequence of the 15/27/28 GHRH plasmid.
US-10-359-919A-14

Query Match      30.4%; Score 1603.8; DB 13; Length 3534;
Best Local Similarity 82.8%; Pred. NO. 0;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY 2706 CTAGACGTAATCATGGTCTATAGCTGTTTCCGTCGTGTAATGTTATCGCTCACAATTC 2765
Db 1412 CTTGGCGTAATCATGGTCTATAGCTGTTTCCGTCGTGTAATGTTATCGCTCACAATTC 1471

QY 2766 ACACAAATACGAGCGCGGAACATAAAGTGTAAAGCCCTGGGGTGCCTAATGAGTGAGCTA 2825
Db 1472 ACACAAATACGAGCGCGGAACATAAAGTGTAAAGCCCTGGGGTGCCTAATGAGTGAGCTA 1531

QY 2826 ACTCACATTAATTCGTTGCGTCACTGCGCGCTTTCAGTCGCGAAACCTGTCGTGCCA 2885
Db 1532 ACTCACATTAATTCGTTGCGTCACTGCGCGCTTTCAGTCGCGAAACCTGTCGTGCCA 1591

QY 2886 GCTGCATTAATGAATCGGCCAAACGCGCGGAGGCGGTTTTCGTTATTCGGCGCTCTTC 2945
Db 1592 GCTGCATTAATGAATCGGCCAAACGCGCGGAGGCGGTTTTCGTTATTCGGCGCTCTTC 1651

QY 2946 CGCTTCCTCGCTCACTGACTCGTTCGCTCGGTTCGTTTCGCTGCGGAGCGGTATCAGC 3005
Db 1652 CGCTTCCTCGCTCACTGACTCGTTCGCTCGGTTCGTTTCGCTGCGGAGCGGTATCAGC 1711

QY 3006 TCACCTCAAGGCGGTAAATACGGTATACCAAGAAATCAGGGGATAACGACGAAAGACAT 3065
Db 1712 TCACCTCAAGGCGGTAAATACGGTATACCAAGAAATCAGGGGATAACGACGAAAGACAT 1771

QY 3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCCGCTTTCGTCGCGTTT 3125
Db 1772 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCCGCTTTCGTCGCGTTT 1831

QY 3126 CCATAGGCTCGGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGG 3185
Db 1832 CCATAGGCTCGGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGG 1891

QY 3186 AAACCCGACAGGACTATAAGATACAGGCGTTTCCCTGTAAGGTCCCTGTCGCTC 3245
Db 1892 AAACCCGACAGGACTATAAGATACAGGCGTTTCCCTGTAAGGTCCCTGTCGCTC 1951

QY 3246 TCCTGTTCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTTCCTCCCTTCGGGAGCGT 3305
Db 1952 TCCTGTTCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTTCCTCCCTTCGGGAGCGT 2011

QY 3306 GCGGCTTTCCTATAGCTACGCTGAGGTATCTCAGTTCGCTGAGGTGCTTCGCTCCAA 3365
Db 2012 GCGGCTTTCCTATAGCTACGCTGAGGTATCTCAGTTCGCTGAGGTGCTTCGCTCCAA 2071

QY 3366 GCTGCGCTGTGTCAGCAACCCCGTTTACGCGGACGCTGCGCTTATCCGGTAACCTA 3425
Db 2072 GCTGCGCTGTGTCAGCAACCCCGTTTACGCGGACGCTGCGCTTATCCGGTAACCTA 2131

QY 3426 TCGTCTTGAGTCCAAACCCCGTAAAGACACGACTTATCGCCACTGGCAGGACCACTGGTAA 3485
Db 2132 TCGTCTTGAGTCCAAACCCCGTAAAGACACGACTTATCGCCACTGGCAGGACCACTGGTAA 2191

QY 3486 CAGGATTAAGCAGGAGGTATGTAGGCGGTGCTACAGAGTTCCTTGAAGTGTGCGCTAA 3545
Db 2192 CAGGATTAAGCAGGAGGTATGTAGGCGGTGCTACAGAGTTCCTTGAAGTGTGCGCTAA 2251

QY 3546 CTACGGCTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAAGCCAGTTACCTT 3605
Db 2252 CTACGGCTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAAGCCAGTTACCTT 2311

QY 3606 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCCCGCTGGTAGCGGTGGTTT 3665
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Db 2312 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCCCGCTGGTAGCGGTGGTTT 2371
QY 3666 TTTTGTGTTGCAAGCAGAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTTTTGAT 3725
Db 2372 TTTTGTGTTGCAAGCAGAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTTTTGAT 2431
QY 3726 CTTTTCCTACGGGTCTGACGCTCAGTGGAAAGAACTCAGTTAAGGATTTTGGTCAAT 3785
Db 2432 CTTTTCCTACGGGTCTGAA----- 2449
QY 3786 GAGATTATCGTCGACCAAGCGGCATCGTGCTCTCCCACTCCTCGAGTTCCGGGGCATG 3845
Db 2450 ----- 2449
QY 3846 GATCGCGGATAGCGCTGCTGTTTCTTGATCCGACCGGATTTGCATCTCCGCGTGA 3905
Db 2450 ----- 2449
QY 3906 CTCGCGAGGTCGTCAGCCTCAGCAGCAGCTGAACCAACTCCGAGGGGATCGAGGCC 3965
Db 2450 ----- 2449
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Db 2450 ----- 2449
QY 4026 CCGGAAAAAGATTCCGAAAGCCAACTTTTATAGAAAGCGCGGTGGAATCGAAATCTCG 4085
Db 2450 ----- 2449
QY 4086 TGATGCGAGTTGGCGCTCGCTTGGTTCGTCATTTTGAACCCAGAGATCCCGCTCAGAG 4145
Db 2450 ----- 2459
QY 4146 AACTCCTCAAGAGGCGATAGAAAGGCGATCGCGTGCAGAACTGGAGCGGATACCGTAA 4205
Db 2460 AACTCCTCAAGAGGCGATAGAAAGGCGATCGCGTGCAGAACTGGAGCGGATACCGTAA 2519
QY 4206 AGCACAGGAGCGGTACGCCCATTTCCGCCCAAGCTTTCAGCAATATCACGGGTAGCC 4265
Db 2520 AGCACAGGAGCGGTACGCCCATTTCCGCCCAAGCTTTCAGCAATATCACGGGTAGCC 2579
QY 4266 AAGCGCTATGCTCTGATAGCGTCCGCGCACACCCAGCGCGCCACAGTCCGATGATCCAGAA 4325
Db 2580 AAGCGCTATGCTCTGATAGCGTCCGCGCACACCCAGCGCGCCACAGTCCGATGATCCAGAA 4385
QY 4326 AAGCGGCCATTTTCCACCAATGATATTCGGCAAGCAGGCAATCGCCATGGGTTCAGCAGAGA 2639
Db 2640 AAGCGGCCATTTTCCACCAATGATATTCGGCAAGCAGGCAATCGCCATGGGTTCAGCAGAGA 2699
QY 4386 TCCTCGCGTCCGGCATCGCGCTTGGCTTGGGCAACAGTTCGGCTCGCGCGAGGCC 4445
Db 2700 TCCTCGCGTCCGGCATCGCGCTTGGCTTGGGCAACAGTTCGGCTCGCGCGAGGCC 2759
QY 4446 TGATGCTCTTCTGCTCAGATCATCTCTGATCGCAACAGCGGCTTCCATCCGAGTACGTGT 4505
Db 2760 TGATGCTCTTCTGCTCAGATCATCTCTGATCGCAACAGCGGCTTCCATCCGAGTACGTGT 2819
QY 4506 CGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCCGATCAAGCGGTATGC 4565
Db 2820 CGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCCGATCAAGCGGTATGC 2879
QY 4566 AGCGCGCGATTTGATCAGCCATGATGATATTTCTCGGAGGAGCAAGGTGAGATGAC 4625
Db 2880 AGCGCGCGATTTGATCAGCCATGATGATATTTCTCGGAGGAGCAAGGTGAGATGAC 2939
QY 4626 AGGAGATCCTCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAGTGACA 4685
Db 2940 AGGAGATCCTCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAGTGACA 2999
QY 4686 ACGTGAGCAGACTGCGCAAGGAAACGCCCTCGTGGCCAGCCAGATAGCCGCGCTGCC 4745
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Db 2450 ----- 2449
QY 4086 TGATGGCAGGTTGGCGCTGCTTGTGTCGTCATTTTGAACCCAGAGTCCCGCTCAGAAG 4145
Db 2450 -----CGCTCAGAAG 2459
QY 4146 AACTCGTCAAGAAGCGGATAGAAGCGGATGCGCTCGGAATCGGAGCGGCGATACCGTAA 4205
Db 2460 AACTCGTCAAGAAGCGGATAGAAGCGGATGCGCTCGGAATCGGAGCGGCGATACCGTAA 2519
QY 4206 AGCAGGAGAAAGCGGTAGCCCATTCGCGCGCAAGCTCTTCAGCAATATCAGGGTAGCC 4265
Db 2520 AGCAGGAGAAAGCGGTAGCCCATTCGCGCGCAAGCTCTTCAGCAATATCAGGGTAGCC 2579
QY 4266 AACCTATGTCTCATAGCGGTGCGCACAACCCAGCGCGCCACAGTTCGATGAATCCAGAA 4325
Db 2580 AACCTATGTCTCATAGCGGTGCGCACAACCCAGCGCGCCACAGTTCGATGAATCCAGAA 2639
QY 4326 AAGCGGCGCATTTCCACCATGATATTCGGCAAGCAGGCGATCGCCATGGGTCAAGCAGAGA 4385
Db 2640 AAGCGGCGCATTTCCACCATGATATTCGGCAAGCAGGCGATCGCCATGGGTCAAGCAGAGA 2699
QY 4386 TCCTCGCGGTGGCGCATCGCGCTTGAGCCTGGCGAACAAGTTCGGGTGGCGCAGCGCC 4445
Db 2700 TCCTCGCGGTGGCGCATCGCGCTTGAGCCTGGCGAACAAGTTCGGGTGGCGCAGCGCC 2759
QY 4446 TGAATGCTCTTTCGTCAGATCATCTGATCGCAAGAAGCGGCTTCATCCGAGTAGTGCT 4505
Db 2760 TGAATGCTCTTTCGTCAGATCATCTGATCGCAAGAAGCGGCTTCATCCGAGTAGTGCT 2819
QY 4506 CGTTCGATCGATGTTTCGCTTGCTGCTCGAATGGCGAGGTAGCGGATCAAGGCTATGC 4565
Db 2820 CGTTCGATCGATGTTTCGCTTGCTGCTCGAATGGCGAGGTAGCGGATCAAGGCTATGC 2879
QY 4566 AGCGCGCGCATTCATCAGCGCATGATGATATCTTCGCGAGGAGCAAGTTCAGTGACA 4625
Db 2880 AGCGCGCGCATTCATCAGCGCATGATGATATCTTCGCGAGGAGCAAGTTCAGTGACA 2939
QY 4626 AGGAGATCTTCCCGCGCATCTCGCCCAATAGCAGCGAGTCCCTTCCTCGCTTCAGTGACA 4685
Db 2940 AGGAGATCTTCCCGCGCATCTCGCCCAATAGCAGCGAGTCCCTTCCTCGCTTCAGTGACA 2999
QY 4686 ACCTCGAGCAGTTCGCGCAAGAAACGCGCTGCTGGCGAGCAAGTTCAGTGAGTGC 4745
Db 3000 ACCTCGAGCAGTTCGCGCAAGAAACGCGCTGCTGGCGAGCAAGTTCAGTGAGTGC 3059
QY 4746 TGTCTCTGAGTTCATTCAGGCGCACCGGACAGGTCTGTCGATCAAAAGAAACCGGCGC 4805
Db 3060 TGTCTCTGAGTTCATTCAGGCGCACCGGACAGGTCTGTCGATCAAAAGAAACCGGCGC 3119
QY 4806 CCCTGCGCTGACAGCGGAAACAGCGGCGCATCAGAGCGCGATTCGTGTGTCGCCAG 4865
Db 3120 CCCTGCGCTGACAGCGGAAACAGCGGCGCATCAGAGCGCGATTCGTGTGTCGCCAG 3179
QY 4866 TCATAGCCGAATAGCTCTCCACCCAGCGCGGAGACCTCGCTGCAATCCATCTTGT 4925
Db 3180 TCATAGCCGAATAGCTCTCCACCCAGCGCGGAGACCTCGCTGCAATCCATCTTGT 3239
QY 4926 TCAATCATCGAAACGATCCTCATCTCTGTCCTTGTATCAGATCTTGATCCCTGCGCCAT 4985
Db 3240 TCAATCATCGAAACGATCCTCATCTCTGTCCTTGTATCAGATCTTGATCCCTGCGCCAT 3299
QY 4986 CAGATCTTGGCGGCAAGAAAGCATTCAGTTTACCTTTCAGGGCTTCCCAACCTTACCA 5045
Db 3300 CAGATCTTGGCGGCAAGAAAGCATTCAGTTTACCTTTCAGGGCTTCCCAACCTTACCA 3359
QY 5046 GAGGCGCGCCAGCTGGCAATTCGGTTCGCTGCTGCTGCTTCCATAAAGCCCGCAGTCTAGC 5105
Db 3360 GAGGCGCGCCAGCTGGCAATTCGGTTCGCTGCTGCTGCTTCCATAAAGCCCGCAGTCTAGC 3419
QY 5106 TATGCCCATGTAAGGCCCATCTGCAAGCTACTCTCTTCTTCTT 5146
Db 3420 AACTGTTGGGAAGGCGATCGGTGGGCGCTCTTCGCTATT 3460
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RESULT 12

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US-10-315-907A-11
; Sequence 11, Application US/10315907A
; Publication No. US20040057941A1
; GENERAL INFORMATION:
; APPLICANT: Advlvsys
; TITLE OF INVENTION: PLASMID MEDIATED SUPPLEMENTATION FOR TREATING CHRONICALLY ILL SUB.
; FILE REFERENCE: 108328.00073 - AVSI-0007
; CURRENT APPLICATION NUMBER: US/10/315.907A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Operatively linked components of the HV-GHRH plasmid.
US-10-315-907A-11
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Query Match 30.4%; Score 1603.8; DB 13; Length 3534;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY 2706 CTAGACGTAATCATGCTCATAGCTGTTTCTGTGTGAAATGTTATCGGTCAAAATCC 2765
Db 1412 CTTGGCGTAATCATGCTCATAGCTGTTTCTGTGTGAAATGTTATCGGTCAAAATCC 1471
QY 2766 ACACAAATACGAGCGGAAAGCATAAAGTGTAAAGCCTGGGGTCCCTAAATGAGTGAGTA 2825
Db 1472 ACACAAATACGAGCGGAAAGCATAAAGTGTAAAGCCTGGGGTCCCTAAATGAGTGAGTA 1531
QY 2826 ACTACATTAATTCGTTGCGTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCA 2885
Db 1532 ACTACATTAATTCGTTGCGTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCA 1591
QY 2886 GCTGCAATTAATGATCGGCAACGCGGGGAGGCGGTTTGGTATTCGGGCGCTCTTC 2945
Db 1592 GCTGCAATTAATGATCGGCAACGCGGGGAGGCGGTTTGGTATTCGGGCGCTCTTC 1651
QY 2946 CGTTCTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 1651
Db 1652 CGTTCTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3005
QY 3006 TCACTCAAAAGGCGTAAATACGGTTATCCACAGAAATCAGGGGATAACGAGGAAAGAACAT 3065
Db 1712 TCACTCAAAAGGCGTAAATACGGTTATCCACAGAAATCAGGGGATAACGAGGAAAGAACAT 1771
QY 3066 GTGAGCAAAAGGCGCAAAAGGCGCAAGAACCGTAAAGGCGCGCTTGTGCGGTTTTT 3125
Db 1772 GTGAGCAAAAGGCGCAAAAGGCGCAAGAACCGTAAAGGCGCGCTTGTGCGGTTTTT 1831
QY 3126 CCATAGGCTCCGCGCGCTGACGAGCATCACAAAATTCAGCGTCAAGTCAGAGTGGCG 3185
Db 1832 CCATAGGCTCCGCGCGCTGACGAGCATCACAAAATTCAGCGTCAAGTCAGAGTGGCG 1891
QY 3186 AAACCGCAGAGCACTATAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTGTGCGCTC 3245
Db 1892 AAACCGCAGAGCACTATAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTGTGCGCTC 1951
QY 3246 TCCTGTTCCGACCTCGCGCTTACCGGATACCTGTGCGGCTTTCCTTCCTTCGGAGCGT 3305
Db 1952 TCCTGTTCCGACCTCGCGCTTACCGGATACCTGTGCGGCTTTCCTTCCTTCGGAGCGT 2011
QY 3306 GCGGCTTCTCATAGCTCAGCGTGTAGTATCTCATGTTCCGTTAGTGTAGTGTTCGTTCC 3365
Db 2012 GCGGCTTCTCATAGCTCAGCGTGTAGTATCTCATGTTCCGTTAGTGTAGTGTTCGTTCC 2071
QY 3366 GCTGGGCTGTGTGACGAAACCCCGCTTTCAGCGGCGGCTTTCAGCGGCTTTCGTTAGTGT 3425
Db 2072 GCTGGGCTGTGTGACGAAACCCCGCTTTCAGCGGCGGCTTTCAGCGGCTTTCGTTAGTGT 2131
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4506	CGCTCGATGCGATGTTTCCTGCTCGTGCAGATGGGACAGTACCGGATCAACGCTATGC	4565
2820	CGCTCGATGCGATGTTTCCTGCTCGTGCAGATGGGACAGTACCGGATCAACGCTATGC	2879
4566	AGCGCGCGCATTCGATCAGCGCATGATGGATCTTTCTCGCAGAGCAAGGTGAGATGAC	4625
2880	AGCGCGCGCATTCGATCAGCGCATGATGGATCTTTCTCGCAGAGCAAGGTGAGATGAC	2939
4626	AGGAGATCTTGCCTCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA	4685
2940	AGGAGATCTTGCCTCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA	2999
4686	ACGTTCGAGACACAGCTGCGCAAGGAACCCCGTCTGTGCGCAGCCACGATAGCGCGCTGCC	4745
3000	ACGTTCGAGACACAGCTGCGCAAGGAACCCCGTCTGTGCGCAGCCACGATAGCGCGCTGCC	3059
4746	TCGTCTCTGCAGTTCAATTCAGGGCACCGGACAGCTCGGTCTTGACAAAAGAACCGGGCGC	4805
3060	TCGTCTCTGCAGTTCAATTCAGGGCACCGGACAGCTCGGTCTTGACAAAAGAACCGGGCGC	3119
4806	CCCTGCGCTGACACCGCGGACACAGCGCGCATCAGAGCAGCGGATTTGCTGTGTGCCGAG	4865
3120	CCCTGCGCTGACACCGCGGACACAGCGCGCATCAGAGCAGCGGATTTGCTGTGTGCCGAG	3179
4866	TCATAGCGGAATAGCCTCTCCACCAACGCGGCCGGAGAACTGGTGGCAATCCCATCTTGT	4925
3180	TCATAGCGGAATAGCCTCTCCACCAACGCGGCCGGAGAACTGGTGGCAATCCCATCTTGT	3239
4926	TCAATTCGCGAAAGCATCTCTCATCTGTCCTTGATCAGATCTTGATCCCTCGCCCAT	4985
3240	TCAATTCGCGAAAGCATCTCTCATCTGTCCTTGATCAGATCTTGATCCCTCGCCCAT	3299
4986	CAGATCTTGGCGGCAAGAAAGCCATCCAGATTTACTTTGCGAGGCTTCCCAACCTTAACA	5045
3300	CAGATCTTGGCGGCAAGAAAGCCATCCAGATTTACTTTGCGAGGCTTCCCAACCTTAACA	3359
5046	GAGGCGGCCACAGCTGGCAATTCCGGTTGCTTGTCTGCATATAAACCGCCAGTCTAGC	5105
3360	GAGGCGGCCACAGCTGGCAATTCCGGTTGCTTGTCTGCATATAAACCGCCAGTCTAGC	3419
5106	TATCGCATGTAAAGCCCACTCAAGCTACCTGCTTTCTCTT	5146
3420	AACTGTGTGGAGAGGGCGATCGGTGCGGGCTCTTTGCTATT	3460

RESULT 13

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US-10-315-907A-12
; Sequence 12, Application US/10315907A
; Publication No. US20040057941A1
; GENERAL INFORMATION:
; APPLICANT: AdvIsys
; TITLE OF INVENTION: PLASMID MEDIATED SUPPLE
; FILE REFERENCE: 108328.00073 - AVSI-0007
; CURRENT APPLICATION NUMBER: US/10/315,907A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; US-10-315-907A-12

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Query Match	30.4%;	Score 1603.8;	DB 13;	Length 3534;
Best local Similarity	82.8%;	Pred. No. 0;		
Matches 202;	Conservative	0;	Mismatches 27;	Indels 392; Gaps 1;
2706	CTAGAGCTAATCATGTCATAGCTGTTTCTCTGTGCAATTTCTATCCGTCACAAATCC	2765		
1412	CTTGGCGTAATCATGTCATAGCTGTTTCTCTGTGCAATTTCTATCCGTCACAAATCC	1471		

3426	QY	TCGCTTTGAGTCCAAACCGGTTAGACACGACTTATCGCCACTCGCAGCAGCCACTGGTAA	3485
2132	Db	TCGCTTTGAGTCCAAACCGGTTAGACACGACTTATCGCCACTCGCAGCAGCCACTGGTAA	2191
3486	QY	CAGGATTAGCAGAGCAGGATGTAGCGGTGTCTACAGAGTTCTTGAAGTGTGGCTAA	3545
2192	Db	CAGGATTAGCAGAGCAGGATGTAGCGGTGTCTACAGAGTTCTTGAAGTGTGGCTAA	2251
3546	QY	CTACGGCTACACTAGAGAAACAGTATTGTGTATCTGGCTCTGCTGAAGCCAGTACCTT	3605
2252	Db	CTACGGCTACACTAGAGAAACAGTATTGTGTATCTGGCTCTGCTGAAGCCAGTACCTT	2311
3606	QY	CGGAAAAAGAGTTGGTAGCTCTTCATCCGGCAAAACCAACCCGCTGCTAGCGGTGTT	3665
2312	Db	CGGAAAAAGAGTTGGTAGCTCTTCATCCGGCAAAACCAACCCGCTGCTAGCGGTGTT	2371
3666	QY	TTTTGTTTGCACGACGAGATACCGCGAGAAAAAAGGATCTCAAGAGATCCTTTGAT	3725
2372	Db	TTTTGTTTGCACGACGAGATACCGCGAGAAAAAAGGATCTCAAGAGATCCTTTGAT	2431
3726	QY	CTTTTCTACGGGCTCTGAGCTCAGTGTGAACGAAAACTCAAGTTAAGGATTTTGTGTCAT	3785
2432	Db	CTTTTCTACGGGCTCTGAGCTCAGTGTGAACGAAAACTCAAGTTAAGGATTTTGTGTCAT	2449
3786	QY	GAGATTATCGTCGACAAAGCGGCATCGTGCCTCCCACTCTCTGCAGTTCTGGGGCATG	3845
2450	Db	-----	2449
3846	QY	GATGCGCGGATAGCGCGCTCCTCGTTTCTTGATGCCAGCGATTTCACCTCCCGGTAGAA	3905
2450	Db	-----	2449
3906	QY	CTCCGCGAGTCTGTCAGCCTCAGGCAGCAGCTGAACCACTCCTCGAGGGGATCGAGCC	3965
2450	Db	-----	2449
3966	QY	GGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCACCGCGGTC	4025
2450	Db	-----	2449
4026	QY	CCGAAAAACGATTCGAAAGCCCAACCTTTTCATAGAAGCGCGGTGAATCGAAATCTCG	4085
2450	Db	-----	2449
4086	QY	TGATGGCAGTTGGGGTCTGCTTTGTCGGTCAATTTGAAACCCAGTCCCGCTCAGAG	4145
2450	Db	-----	2459
4146	QY	AATCTGTCAGAGAGCGGATAGAGGCGATCGCTCGAATCGGAGCGCGCATCCGTAA	4205
2460	Db	AATCTGTCAGAGAGCGGATAGAGGCGGATCGCTCGAATCGGAGCGCGCATCCGTAA	2519
4206	QY	AGCAGAGGAAGCGGTACAGCCATTCCGCCCAAGCTCTTCAGCAATATCACGGGTAGCC	4265
2520	Db	AGCAGAGGAAGCGGTACAGCCATTCCGCCCAAGCTCTTCAGCAATATCACGGGTAGCC	2579
4266	QY	AACGCTATGCTGATAGCGGTCCGCCACACCCAGCGCGCCACAGTCGATGATCCAGAA	4325
2580	Db	AACGCTATGCTGATAGCGGTCCGCCACACCCAGCGCGCCACAGTCGATGATCCAGAA	2639
4326	QY	AAGCGGCATTTTCCACCATGATATTCGCAAGCAGGCATCGCATGGGTACAGCAGAA	4385
2640	Db	AAGCGGCATTTTCCACCATGATATTCGCAAGCAGGCATCGCATGGGTACAGCAGAA	2699
4386	QY	TCCTCGCGGTGGGCATCGCGCTTGAGCTTCGGCAACAGATTTCGGCTGGCGGAGCCCC	4445
2700	Db	TCCTCGCGGTGGGCATCGCGCTTGAGCTTCGGCAACAGATTTCGGCTGGCGGAGCCCC	2759
4446	QY	TGATGCTCTTCGTCAGATCATCTGATTCAGACAGACCGGCTTCCATCCGAGTACGTGCT	4505
2760	Db	TGATGCTCTTCGTCAGATCATCTGATTCAGACAGACCGGCTTCCATCCGAGTACGTGCT	2819

QY	2766	ACACAACATACGAGCCGGAAGCATAAAGTCTAAAGCCTGGGGTGCCTTAATGAGTGAGCTA	2825	Db	2450	-----	2449
Db	1472	ACACAACATACGAGCCGGAAGCATAAAGTCTAAAGCCTGGGGTGCCTTAATGAGTGAGCTA	1531	QY	3906	CTCCGCGAGGTCGTCCAGCCTCAGGCAGCAGCTGAAACAACTCGCGAGGGGATCGAGCC	3965
QY	2826	ACTCACATTAATGCGTTGCGCTCACTCCCGCTTTCCAGTCGGGAAACCTGTGTCGCA	2885	Db	2450	-----	2449
Db	1532	ACTCACATTAATGCGTTGCGCTCACTCCCGCTTTCCAGTCGGGAAACCTGTGTCGCA	1591	QY	3966	GGGCTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGGCGTC	4025
QY	2886	GCTGCATTAATGAATCGGCCAAACGCGGGGAGAGCGGTTTGCGTATTTGGGCGCTCTTC	2945	Db	2450	-----	2449
Db	1592	GCTGCATTAATGAATCGGCCAAACGCGGGGAGAGCGGTTTGCGTATTTGGGCGCTCTTC	1651	QY	4026	CCGAAAAACGATTCGAAAGCCAACTTTTATAGAAAGCGCGGTGGAATCGAAATCTCG	4085
QY	2946	CGCTTCCTCGCTCACTGACTCGCTCGCTCGGTTCGCTCGGCTCGGCGAGCGGTATCAGC	3005	Db	2450	-----	2449
Db	1652	CGCTTCCTCGCTCACTGACTCGCTCGCTCGGTTCGCTCGGCTCGGCGAGCGGTATCAGC	1711	QY	4086	TGATGGCAGGTTGGGCGCTCGCTTGGTTCGCTCATTTTCGAAACCCAGAGTCCCGCTCAGAAG	4145
QY	3006	TCACTCAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACCGAGGAAGACAT	3065	Db	2450	-----	2459
Db	1712	TCACTCAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACCGAGGAAGACAT	1771	QY	4146	AACCTCGTCAAGAGCGGATAGAGCGCATGGCTGCGAATCGGAGCGGCGATACCGTAA	4205
QY	3066	GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTT	3125	Db	2460	AACCTCGTCAAGAGCGGATAGAGCGCATGGCTGCGAATCGGAGCGGCGATACCGTAA	2519
Db	1772	GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTT	1831	QY	4206	AGCACGAGGAAGCGGTCAAGCCCATTTCCCGCCCAAGCTCTTCAGCAATATCACGGGTAGCC	4265
QY	3126	CCATAGGCTCGCCCGCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGTGGCG	3185	Db	2520	AGCACGAGGAAGCGGTCAAGCCCATTTCCCGCCCAAGCTCTTCAGCAATATCACGGGTAGCC	2579
Db	1832	CCATAGGCTCGCCCGCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGTGGCG	1891	QY	4266	AACGCTATGCTGTATGAGCGGTCCGCCACACCCAGCGCGGCAACAGTCGATGAATCCAGAA	4325
QY	3186	AAACCCGACAGGACTATAAAGATACAGGCGTTTCCCGCTTGGAGCTCCCTCGTGGCTC	3245	Db	2580	AACGCTATGCTGTATGAGCGGTCCGCCACACCCAGCGCGGCAACAGTCGATGAATCCAGAA	2639
Db	1892	AAACCCGACAGGACTATAAAGATACAGGCGTTTCCCGCTTGGAGCTCCCTCGTGGCTC	1951	QY	4326	AAGCGGCCATTTTCCACCATGATATTGGCAAGCAGCATCGCATGGGTCAAGACGAGA	4385
QY	3246	TCTGTTCGACCGCTGCGCTTACCGGATACCTGTGCGGCTTCTCCCTTCGGGAAGCGT	3305	Db	2640	AAGCGGCCATTTTCCACCATGATATTGGCAAGCAGCATCGCATGGGTCAAGACGAGA	2699
Db	1952	TCTGTTCGACCGCTGCGCTTACCGGATACCTGTGCGGCTTCTCCCTTCGGGAAGCGT	2011	QY	4386	TCCTCGCGCTCGGCGCATGCGCGCTTTCGAGCTTCGCGGCAACAGTTTCGGCTCGCGGAGCCCC	4445
QY	3306	GGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTGTGCTTCGCTCAA	3365	Db	2700	TCCTCGCGCTCGGCGCATGCGCGCTTTCGAGCTTCGCGGCAACAGTTTCGGCTCGCGGAGCCCC	2759
Db	2012	GGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGTGTGCTTCGCTCAA	2071	QY	4446	TGATGCTTCTGCTCAGATCATCTGANTCGAAGACCGGCTTCCATTCGAGTACGTGCT	4505
QY	3366	GCTGGGCTGTGTGACGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCCGTAACTA	3425	Db	2760	TGATGCTTCTGCTCAGATCATCTGANTCGAAGACCGGCTTCCATTCGAGTACGTGCT	2819
Db	2072	GCTGGGCTGTGTGACGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCCGTAACTA	2131	QY	4506	CGCTCCATCGATGTTTTCGCTTGGTGTGATGGGAGGTAGCCGATCAAGCGGTATGC	4565
QY	3426	TCGCTTTGAGTCAACCCCGTAAAGACACGACTTATCGCCACTGGCAGCCTACTGTAA	3485	Db	2820	CGCTCCATCGATGTTTTCGCTTGGTGTGATGGGAGGTAGCCGATCAAGCGGTATGC	2879
Db	2132	TCGCTTTGAGTCAACCCCGTAAAGACACGACTTATCGCCACTGGCAGCCTACTGTAA	2191	QY	4566	AGCCGCGCATTTGCATCAGCCATGATGATATCTTCTCGGAGGAGCAAGGTGAGATGAC	4625
QY	3486	CAGGATTCAGAGCGAGGTATGAGCGGTGCTACAGAGTTCTTGAAGTGTGGCTAA	3545	Db	2880	AGCCGCGCATTTGCATCAGCCATGATGATATCTTCTCGGAGGAGCAAGGTGAGATGAC	2939
Db	2192	CAGGATTCAGAGCGAGGTATGAGCGGTGCTACAGAGTTCTTGAAGTGTGGCTAA	2251	QY	4626	AGGAGATCTTGCCTCCGCGCATTTGCGCCCAATAGACGCACTCCCTTCCCGTTCAGTGACA	4685
QY	3546	CTACGGCTACCTAGAGAAACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTT	3605	Db	2940	AGGAGATCTTGCCTCCGCGCATTTGCGCCCAATAGACGCACTCCCTTCCCGTTCAGTGACA	2999
Db	2252	CTACGGCTACCTAGAGAAACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTT	2311	QY	4686	AGTTCGAGCACAGCTCGGCAAGAACCGCCGCTGTTGGCCAGCCACCATAGCCGCTGCC	4745
QY	3606	CGGAAAAAGAGTTGTAGTCTTTGATCCGGCAAAACAAACCCGCTGTTAGCGGTGGTTT	3665	Db	3000	AGTTCGAGCACAGCTCGGCAAGAACCGCCGCTGTTGGCCAGCCACCATAGCCGCTGCC	3059
Db	2312	CGGAAAAAGAGTTGTAGTCTTTGATCCGGCAAAACAAACCCGCTGTTAGCGGTGGTTT	2371	QY	4746	TCGTCCTGCACTTCAATTCAGGGCACCGGACAGCTCGGTCTTGACAAAAAGAACCGGGCGC	4805
QY	3666	TTTTTTTTCAGAGCAGCAGTACCGGCGAGAAAAAGGATCTCAAGAGATCTTTTGAT	3725	Db	3060	TCGTCCTGCACTTCAATTCAGGGCACCGGACAGCTCGGTCTTGACAAAAAGAACCGGGCGC	3119
Db	2372	TTTTTTTTCAGAGCAGCAGTACCGGCGAGAAAAAGGATCTCAAGAGATCTTTTGAT	2431	QY	4806	CCCTCGGCTGACAGCGGAAACCGGGCGCATCAGAGCCCGGATGTCGTTGTGCCAG	4865
QY	3726	CTTTTCTACGGGCTGTACGCTCAGTGGAAACGAAACCTCACGTTTAAAGGATTTGTCAT	3785	Db	3120	CCCTCGGCTGACAGCGGAAACCGGGCGCATCAGAGCCCGGATGTCGTTGTGCCAG	3179
Db	2432	CTTTTCTACGGGCTGTACGCTCAGTGGAAACGAAACCTCACGTTTAAAGGATTTGTCAT	2499	QY	4866	TCATAGCCGAATAGCCTCTCCACCCAAAGCGCGGAGAACCTTGCCTGCAATCACTTGT	4925
QY	3786	GAGATTATCGTCAACAAAGCGGCCATCGTGCTCCCGCTCCCGCTCCCGCTCCCGCT	3845	Db	3180	TCATAGCCGAATAGCCTCTCCACCCAAAGCGCGGAGAACCTTGCCTGCAATCACTTGT	3239
Db	2450	-----	2449	QY	4926	TCATAGCCGAATAGCCTCTCCACCCAAAGCGCGGAGAACCTTGCCTGCAATCACTTGT	4985
QY	3846	GATCGCGGATAGCGCTGCTGTTTCTGATGCGGACGGATTTGCACTGCGGTAGAA	3905				

Db 3240 TCAATCATGCGAAGCATCTCATCTCTCTTGTATCAGATCTTGATCCCTCGGCCAT 3299
QY 4986 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTGCAGGGCTTCCCAACCTTACCA 5045
Db 3300 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTGCAGGGCTTCCCAACCTTACCA 3359
QY 5046 GAGGCGCCCGCAGTGGCAATTCGGTTCGCTGTGTCCTCAATAAACCGCCAGTCTAGC 5105
Db 3360 GAGGCGCCCGCAGTGGCAATTCGGTTCGCTGTGTCCTCAATAAACCGCCAGTCTAGC 3419
QY 5106 TATGCCATGTAAGCCCACTCAAGCTACCTGCTTCTCTT 5146
Db 3420 AACTTTGGGAAGGCGATCGGTGGGGCTCTTCGCTATT 3460

RESULT 14
US-10-315-907A-13
; Sequence 13, Application US/10315907A
; Publication No. US20040057941A1
; GENERAL INFORMATION:
; APPLICANT: Advisys
; TITLE OF INVENTION: PLASMID MEDIATED SUPPLEMENTATION FOR TREATING CHRONICALLY ILL SUB
; FILE REFERENCE: 108328.00073 - AVSI-0007
; CURRENT APPLICATION NUMBER: US/10/315,907A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Operatively linked components of the TV-GHRH plasmid.
US-10-315-907A-13

Query Match 30.4%; Score 1603.8; DB 13; Length 3534;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY 2706 CTAGACGTAATCATGTCTATAGCTGTTTCTCTGTGTGAAATTTGTTATCCGCTCACAATTC 2765
Db 1412 CTITGGGTAAATCATGTCTATAGCTGTTTCTCTGTGTGAAATTTGTTATCCGCTCACAATTC 1471
QY 2766 ACAACAATACGAGCGGCAAGCAATAAGTGAAGCTGGGTGGCTTAATGATGAGCTA 2825
Db 1472 ACAACAATACGAGCGGCAAGCAATAAGTGAAGCTGGGTGGCTTAATGATGAGCTA 1531
QY 2826 ACTCACATTAATGCGTTGCGTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885
Db 1532 ACTCACATTAATGCGTTGCGTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 1591
QY 2886 GCTGCATTAATGAATCGGCCAAGCGCGGGGAGAGCGGTTTTCGTATTGGGCGCTCTTC 2945
Db 1592 GCTGCATTAATGAATCGGCCAAGCGCGGGGAGAGCGGTTTTCGTATTGGGCGCTCTTC 1651
QY 2946 CGTTTCCTCTCACTGACTCGTGTGCGCTCGTGTGCGCTGCGGCGAGCGGTATCAGC 3005
Db 1652 CGTTTCCTCTCACTGACTCGTGTGCGCTCGTGTGCGCTGCGGCGAGCGGTATCAGC 1711
QY 3006 TCACCTAAAGCGGTAATACGTTTATCCACAGATCAGGGGATAACCGAGGAAGAACAT 3065
Db 1712 TCACCTAAAGCGGTAATACGTTTATCCACAGATCAGGGGATAACCGAGGAAGAACAT 1771
QY 3066 GTGAGCAAAAGGCGCAAGAAAGCCAGAACCGTAAAGCCGCGTGTGCTGGGCTTTT 3125
Db 1772 GTGAGCAAAAGGCGCAAGAAAGCCAGAACCGTAAAGCCGCGTGTGCTGGGCTTTT 1831
QY 3126 CCATAGGCTCGGCCCTTACGAGCATCACAAATCGAGCTCAAGTCAGAGTGGCG 3185
Db 1832 CCATAGGCTCGGCCCTTACGAGCATCACAAATCGAGCTCAAGTCAGAGTGGCG 1891
QY 3186 AAACCCGACGAGCTATTAAGATACCAAGCGCTTTCCCGCTGGAAAGCTCCCTCGTGGCTC 3245

Db 1892 AAACCCGACAGCACTATAAGATACCAAGCGTTTCCCGCTGGAAGCTCCCTCGTGGCGTC 1951
QY 3246 TCCTGTTCCGACCTCGCGCTTACCGATACCTGTCCGCCCTTTCTCCCTTCGGGAAGCGT 3305
Db 1952 TCCTGTTCCGACCTCGCGCTTACCGATACCTGTCCGCCCTTTCTCCCTTCGGGAAGCGT 2011
QY 3306 GGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGTGTAGGTTCGTTCCGTC 3365
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QY 3366 GCTGGCTGTGTGACGAAACCCCGCTTACCGCGACCGCTGCGCTTATCCGGTAACCTA 3425
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QY 4566 AGCGCGCGCATGTCATCAGCCATGATGATGATGATGATGATGATGATGATGATGATGATG 4625
Db 2880 AGCGCGCGCATGTCATCAGCCATGATGATGATGATGATGATGATGATGATGATGATGATG 2939
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QY 5046 GAGGCGCGCCAGCTGGCAATTCGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5105
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RESULT 15
US-10-315-907A-14
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; Publication No. US20040057941A1
; GENERAL INFORMATION:
; APPLICANT: Advisys
; TITLE OF INVENTION: PLASMID MEDIATED SUPPLEMENTATION FOR TREATING CHRONICALLY ILL SUB
; FILE REFERENCE: 108328.00073 - AVSI-0007
; CURRENT APPLICATION NUMBER: US/10/315,907A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 3534
; TYPE: DNA
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; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Operatively linked components of the 15/27/28 GHRH plasmid.
US-10-315-907A-14
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Best Local Similarity 82.8%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;
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4866 QY TCATAGCCGAATAGCTCTCCACCCCAAGCGCGGAGAACCTGCGTGCATTCATCCTTTGT 4925
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Search completed: August 4, 2004, 19:57:28
Job time : 2268 secs

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3726 QY CTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCAGTTAAGGGATTTGGTTCAT 3785
2432 Db CTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCAGTTAAGGGATTTGGTTCAT 2449
3786 QY GAGATTATCGTCGACAAAGCGGCATCGTGCTCCCACTCTCTGCAAGTTGCGGGGCATG 3845
2450 Db GAGATTATCGTCGACAAAGCGGCATCGTGCTCCCACTCTCTGCAAGTTGCGGGGCATG 2449
3846 QY GATGCGCGATAGCGCTGCTGTGTTTCTGGAGCCGCGGATTTGCACTGCCGGTAGAA 3905
2450 Db GATGCGCGATAGCGCTGCTGTGTTTCTGGAGCCGCGGATTTGCACTGCCGGTAGAA 2449
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3000 Db ACCTCGAGCAGCTGCGGCAAGGAAACCGCGTTCGTGCGCAGCAGTACCGCGCTGCC 3059
4746 QY TCGTCTGCGATTCATTTCAGGGCACCGGACAGGTCGGTCTTTCACAAAAAGAACCGGGGCGC 4805

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:18:02 ; Search time 12184 Seconds

Title: US-09-921-143-36

Perfect score: 5283

Sequence: 1 aagcttgacctatgcgact.....tgagtgcttgcgcgagcgtg 5283
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_estl:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

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21: em_gss_fun:*

22: em_gss_mam:*

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25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gssl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	991	18.8	2450	11 AK047844	AK047844 Mus muscu
2	948	17.9	1067	9 AU081137	AU081137 Mus muscu
3	939.4	17.8	954	14 CK283361	CK283361 EST746083
4	924.6	17.5	947	14 CK298208	CK298208 EST760922

5	919.8	17.4	1089	9 AU081124	AU081124 AU081124
6	918.6	17.4	935	14 CK284786	CK284786 EST747508
7	911	17.2	936	14 CK256977	CK256977 EST740614
8	907	17.2	910	14 CK287930	CK287930 EST750652
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10	898.8	17.0	996	29 CG392995	CG392995 ZMMBbc000
11	886.4	16.8	933	14 CK291799	CK291799 EST754513
12	883.6	16.7	1021	29 CG392916	CG392916 ZMMBbc000
13	875	16.6	925	14 CB686151	CB686151 Bn01b_02o
14	866.2	16.4	1073	14 CF269652	CF269652 Fcy1col48
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16	843	16.0	856	14 CK287297	CK287297 EST750019
17	814.4	15.4	906	29 CG839354	CG839354 ZMMBbc021
18	809.2	15.3	966	28 BZ570738	BZ570738 msh2_1513
19	803	15.2	804	14 CK291519	CK291519 EST754233
20	794	15.0	811	14 CK288185	CK288185 EST750907
21	781.2	14.8	1163	9 AU081044	AU081044 AU081044
22	781.2	14.8	1249	28 BZ572284	BZ572284 msh2_2572
23	780.8	14.8	831	12 BG680919	BG680919 602628716
24	780.8	14.8	858	14 CA488579	CA488579 AGENCOURT
25	780.6	14.8	833	14 CB686421	CB686421 Bn01b_04j
26	774	14.7	954	9 AU044364	AU044364 DXF2p434C
27	769.2	14.6	863	14 CF752100	CF752100 TGBR9 Hum
28	760.8	14.4	878	14 CK288711	CK288711 EST751433
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41	711	13.5	1004	9 AJ281480	AJ281480 4A3A-P4G8
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ALIGNMENTS

RESULT 1
AK047844

LOCUS

DEFINITION

AK047844 2450 bp mRNA linear HTC 20-SEP-2003
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30004M09 product:vascular endothelial growth factor C, full insert sequence.

ACCESSION

VERSION AK047844.1 GI:26339001

KEYWORDS

SOURCE HTC; CAP trapper.

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE High-efficiency full-length cDNA cloning

JOURNAL

MEDLINE Meth. Enzymol. 303, 19-44 (1999)

REFERENCE

1 10349636

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL

MEDLINE Genome Res. 10 (10), 1617-1630 (2000)

PUBMED 20499374

11042159

callus tissue and root tissue"
/lab_host="DH10B-TorA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site.1: EcoRI; Site.2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Query Match 17.5%; Score 924.6; DB 14; Length 947;
Best Local Similarity 99.6%; Pred. No. 8.7e-215;
Matches 927; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 947 GCTGAGGATCATCAGCGCGTCCCGAAACGATTCCGAAGCCCAACCTTTTCATAGA 888
QY 4061 AGCGCGGTGGAATCGAAATCTCGTATGGAGGATGGCGTTCGCTGGTCAATT 4120
DB 887 AGCGCGGTGGAATCGAAATCTCGTATGGAGGATGGCGTTCGCTGGTCAATT 828
QY 4121 CGAAACCCAGAGTCCCGCTCAGAGAACTCTGTCAGAGGCGATAGAGGCGATCGCGTG 4180
DB 827 CGAAACCCAGAGTCCCGCTCAGAGAACTCTGTCAGAGGCGATAGAGGCGATCGCGTG 768
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DB 707 CTCTTCAGCATATCAGGGTAGCAGAGCTATGTCCTGATAGCGGTCCGACACCCAG 648
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QY 4421 GAACAGTTCGGTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAAG 4480
DB 527 GAACAGTTCGGTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGACAAG 468
QY 4481 ACCGGCTTCATCCGAGTACGTGCTCGTCGATCGATGTTTCCTGTTGGTGGTCAATGG 4540
DB 467 ACCGGCTTCATCCGAGTACGTGCTCGTCGATCGATGTTTCCTGTTGGTGGTCAATGG 408
QY 4541 GACAGTACCGGATCAAGCGGTATGACGCGCGCATTCGATTCAGCCATGATGATATTT 4600
DB 407 GACAGTACCGGATCAAGCGGTATGACGCGCGCATTCGATTCAGCCATGATGATATTT 348
QY 4601 CTGCGCAGGACAGGTGAGATGACAGAGATCTTCGCCCGGCACTTCGCCCAATAGCAG 4660
DB 347 CTGCGCAGGACAGGTGAGATGACAGAGATCTTCGCCCGGCACTTCGCCCAATAGCAG 288
QY 4661 CCAGTCCCTCCCGCTTCAGTGACAGCTCGACACAGCTGCGCAAGAACGCCCGTCTGT 4720
DB 287 CCAGTCCCTCCCGCTTCAGTGACAGCTCGACACAGCTGCGCAAGAACGCCCGTCTGT 228
QY 4721 GGCCAGCCAGATAGCCGCGCTGCTGCTCCTGAGTTCATTCAGGCGCACCGACAGGTC 4780
DB 227 GGCCAGCCAGATAGCCGCGCTGCTGCTCCTGAGTTCATTCAGGCGCACCGACAGGTC 168

QY 4781 GCTCTTGACAAAAAGAACCGCGCCCTGCTGACAGCGGAAACACGCGCATCAGA 4840
DB 167 GCTCTTGACAAAAAGAACCGCGCGCCCTGCTGACAGCGGAAACACGCGCATCAGA 108
QY 4841 GCAGCGGATGCTGCTGTGTGTCAGGATCATAGCGGATAGCCTCTCCACCAAGCGCGG 4900
DB 107 GCAGCGGATGCTGCTGTGTGTCAGGATCATAGCGGATAGCCTCTCCACCAAGCGCGG 48
QY 4901 AGAACCTCGGTCGAATCCATCTTGTTCATC 4931
DB 47 AGAACCTCGGTCGAATCCATCTTGTTCATC 17

RESULT 5
LOCUS AU081124 1089 bp mRNA linear EST 30-JUL-2002
DEFINITION AU081124 Oncorhynchus mykiss Kidney infected by infectious hematopoietic necrosis virus
mRNA sequence.
ACCESSION AU081124 GI:6431472
VERSION AU081124.1
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 1089)
AUTHORS Kono, T., Sakai, M. and LaPatra, S.E.
TITLE Expressed Sequence Tag Analysis of Kidney and Gill Tissues from Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious Hematopoietic Necrosis Virus
JOURNAL Mar. Biotechnol. 2 (5); 493-498 (2001)
COMMENT Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.

FEATURES
Location/Qualifiers
source 1..1089
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="KG'12"
/tissue_type="kidney"
/clone_lib="Oncorhynchus mykiss Kidney infected by infectious hematopoietic necrosis virus"
/notes="common name:rainbow trout ; infected by infectious hematopoietic necrosis virus"

ORIGIN

Query Match 17.4%; Score 919.8; DB 9; Length 1089;
Best Local Similarity 97.2%; Pred. No. 1.4e-213;
Matches 979; Conservative 0; Mismatches 22; Indels 6; Gaps 4;

QY 2706 CTAGACCTAATCATGGTCATAGCTGTTCTCTGCTGTAATGTTATCGGCTCAAAATCC 2765
DB 83 CTGGCGTAATCATGGTCATAGCTGTTCTCTGTAATGTTATCGGCTCAAAATCC 142
QY 2766 ACAACAATACGAGCGGAAAGCATAAAGTGAAGCTGGGTCCTTAATGAGTGAGCTA 2825
DB 143 ACAACAATACGAGCGGAAAGCATAAAGTGAAGCTGGGTCCTTAATGAGTGAGCTA 202
QY 2826 ACTCACATTAATGCGTGGCTCACTGCCGCTTTCAGTCGGGAAACCTGTGTCGCA 2885
DB 203 ACTCACATTAATGCGTGGCTCACTGCCGCTTTCAGTCGGGAAACCTGTGTCGCA 262
QY 2886 GCTGCATTAATGAATCGGCCAACCGCGGAGAGCGGTTTCGATATGGGCGCTCTTC 2945
DB 263 GCTGCATTAATGAATCGGCCAACCGCGGAGAGCGGTTTCGATATGGGCGCTCTTC 322
QY 2946 CGCTTCCTCGCTCACTGACTCGCTCGGTCGCTTCGCTCGGCGAGCGGTATCAGC 3005


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Db      335  |||||GATCTGCCCCGACATTCGCCCAATAGCAGCGAGTCCCTTCCCGCTTCAGTGCAACAGT 276
QY      4690  CGAGCACAGCTCGCGAAGAACGCCCGTGTGGCCAGCCAGCATAGCCCGCTGCTCGT 4749
Db      275  CGAGCACAGCTCGCGAAGAACGCCCGTGTGGCCAGCCAGCATAGCCCGCTGCTCGT 216
QY      4750  CCTGCAGTTCATTCAGGACCGGACAGTCTGGTCTTGACAAAGAACCGGCGCCCT 4809
Db      215  CCTGCAGTTCATTCAGGACCGGACAGTCTGGTCTTGACAAAGAACCGGCGCCCT 156
QY      4810  GCGCTGACAGCCGGAACACGGCGGATCAGACGCGGATCTGTGTCGCCAGTAT 4869
Db      155  GCGCTGACAGCCGGAACACGGCGGATCAGACGCGGATCTGTGTCGCCAGTAT 96
QY      4870  AGCCGAATAGCTCTCCACCCAGCGCGGAGAACCTGCGTGCATCATCTTGTCAA 4929
Db      95  AGCCGAATAGCTCTCCACCCAGCGCGGAGAACCTGCGTGCATCATCTTGTCAA 36
QY      4930  TCATGCGAAACGATCCTCATCTGT 4954
Db      35  TCAITCGAAACGATCCAGATCCGGT 11

RESULT 7
CK256977/c
LOCUS
DEFINITION
EST740614 potato callus cDNA library, linear EST 12-DEC-2003
Solanum tuberosum cDNA clone POCD170 5' end, mRNA sequence.
ACCESSION
CK256977
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 936)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1..936
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCD170"
/tissue_type="callus"
/lab_host="DH10B-Tona"
/clone_lib="potato callus cDNA library, normalized and
full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."

ORIGIN
Query Match 17.2%; Score 911; DB 14; Length 936;
Best Local Similarity 99.9%; Pred. No. 1.9e-211;
Matches 922; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      4010  TCATCCAGCGCGGTGCC-GGAAACGATTCCGAAGCCCAACCTTTTCATAGAAGCGGCG 4068
Db      936  TCATCCAGCGCGGTCCCGGGAACGATTCCGAAGCCCAACCTTTTCATAGAAGCGGCG 877
QY      4069  GTGGAATCGAAATCTCGTGTATGTCAGTTGGGCGTGTGTCGGTCAATTCGAACCCC 4128

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RESULT 8
 CK287930/c
 LOCUS
 DEFINITION
 EST750652 Nicotiana benthamiana mixed tissue cDNA library,
 normalized, full-length Nicotiana benthamiana cDNA clone NBMB75 5',
 end, mRNA sequence.
 CK287930
 CK287930.1 GI:39864940
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Nicotiana benthamiana
 Nicotiana benthamiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Nicotiana.

CK287930 910 bp mRNA linear EST 15-DEC-2003
 EST750652 Nicotiana benthamiana mixed tissue cDNA library,
 normalized, full-length Nicotiana benthamiana cDNA clone NBMB75 5',
 end, mRNA sequence.
 CK287930
 CK287930.1 GI:39864940
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Nicotiana benthamiana
 Nicotiana benthamiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE 1 (bases 1 to 910)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H., and Baker, B.
TITLE Generation of EST sequences from *Nicotiana benthamiana*
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST750653
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ANT TAG CTG ACA CTA TAG.
Location/Qualifiers
1. .910
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBM875"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from *Nicotiana benthamiana*
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (*Pseudomonas syringae* pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 16hr;
Pseudomonas syringae pv phaseolicola 18hr, and *Xanthomonas*
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match 17.2%; Score 907; DB 14; Length 910;
Best Local Similarity 100.0%; Pred. No. 1.7e-210; Indels 0; Gaps 0;
Matches 907; Conservative 0; Mismatches 0

QY 4025 CCGGAAACGATTCCGAAGCCCAACCTTTTCATAGAGGGCGGTGGAATCGAATCTC 4084
DB 910 CCGGAAACGATTCCGAAGCCCAACCTTTTCATAGAGGGCGGTGGAATCGAATCTC 851
QY 4085 GTGATGCAGGTTGGGCGTCTTGGTGGTCAATTCGAACCCAGAGTCCCGTCA 4144
DB 850 GTGATGCAGGTTGGGCGTCTTGGTGGTCAATTCGAACCCAGAGTCCCGTCA 791
QY 4145 GAATCTCTCAAGAGCGATAGAGGCGATCGCTGCGAATCGGAGCGGCGATACGTA 4204
DB 790 GAATCTCTCAAGAGCGGATAGAGGCGATCGCTGCGAATCGGAGCGGCGATACGTA 731
QY 4205 AAGCAGGAGGAGCGGTGAGCCCATTTGCGCCCAAGCTTTTCAGCAATATCACGGTAGC 4264
DB 730 AAGCAGGAGGAGCGGTGAGCCCATTTGCGCCCAAGCTTTTCAGCAATATCACGGTAGC 671
QY 4265 CAACGCTATGTCCTGATAGCGGTGCGGCACACCCAGCGGCCACAGTCGATCCAGA 4324
DB 670 CAACGCTATGTCCTGATAGCGGTGCGGCACACCCAGCGGCCACAGTCGATCCAGA 611
QY 4325 AAAGCGGCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCAACACGAG 4384
DB 610 AAAGCGGCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCAACACGAG 551
QY 4385 ATCCTCGCGGTGCGGCATGCGCGCTTGAGCTGCGCAACAGTTTCGGTGGCGGAGCCC 4444
DB 550 ATCCTCGCGGTGCGGCATGCGCGCTTGAGCTGCGCAACAGTTTCGGTGGCGGAGCCC 491
QY 4445 CTGATGCTCTTCGTCACATATCTCTGATCGACAGCGGCTTCCATCCGAGTACGTC 4504
DB 490 CTGATGCTCTTCGTCACATATCTCTGATCGACAGCGGCTTCCATCCGAGTACGTC 431
QY 4505 TCGCTCGATGCGATGTTTTCGCTTGGTGGTTCGAAATGGGCGAGGTAGCCGGATCAAGCGTATG 4564

Db 430 TCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGCGAGGTAGCCGGATCAAGCGTATG 371
QY 4565 CAGCGCGCGCATTTGCATGAGCCATGATGATATCTTCTCGGAGGAGCAAGGTGAGATGA 4624
Db 370 CAGCGCGCGCATTTGCATGAGCCATGATGATATCTTCTCGGAGGAGCAAGGTGAGATGA 311
QY 4625 CAGGAGATCCTGCCCGGCACCTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGAC 4684
Db 310 CAGGAGATCCTGCCCGGCACCTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTCAGTGAC 251
QY 4685 AACGTCGAGCAGCAGCTGCGCAAGGAGCGCGCTGCTGGCCAGCCACGATAGCGCGCTGC 4744
Db 250 AACGTCGAGCAGCAGCTGCGCAAGGAGCGCGCTGCTGGCCAGCCACGATAGCGCGCTGC 191
QY 4745 CTCGCTCGCTCAGTTCATTTCAGGCGCACCGGACAGGTGCGTCTTGACAAAAGAACCGGGCG 4804
Db 190 CTCGCTCGCTCAGTTCATTTCAGGCGCACCGGACAGGTGCGTCTTGACAAAAGAACCGGGCG 131
QY 4805 CCGCTCGCTGAGCAGCGCGGACACCGCGGCATCAGAGAGCGCGATTCGTCTGTGTGCCCA 4864
Db 130 CCGCTCGCTGAGCAGCGCGGACACCGCGGCATCAGAGAGCGCGATTCGTCTGTGTGCCCA 71
QY 4865 GTCATAGCGCATAGCTCTCCACCCAGCGCGGAGACCTGCGTGAATCCATCTTG 4924
Db 70 GTCATAGCGCATAGCTCTCCACCCAGCGCGGAGAACCTGCGTGAATCCATCTTG 11
QY 4925 TTCAATC 4931
Db 10 TTCAATC 4

RESULT 9
CG700598 1025 bp DNA linear GSS 15-OCT-2003
LOCUS ZMMBHC0120G04f ZMMBHC (EcoRI) Zea mays subsp. mays genomic clone
DEFINITION ZMMBHC0120G04 5', genomic survey sequence.
ACCESSION CG700598
VERSION CG700598.1 GI:37688399
KEYWORDS GSS.
SOURCE Zea mays subsp. mays (maize)
ORGANISM Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1025)
AUTHORS Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
Zohovetz, V., Fuks, S., Yu, Y., Wing, R., and Messing, J.
TITLE Sequencing of the maize genome at FGI (2003c)
JOURNAL Unpublished (2003)
COMMENT Contact: Bharti, A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Freelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 24.
Location/Qualifiers
1. .1025
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/mol_type="genomic DNA"
/cultivar="B73"
/sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMMBHC0120G04"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBHC (EcoRI)"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

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location/Qualifiers
1. .1025
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Query Match	17.0%;	Score 899.6;	DB 29;	Length 1025;
Best Local Similarity	98.2%;	Pred. No. 1.2e-208;		
Matches	931;	Conservative 0;	Mismatches 14;	Indels 3; Gaps 2;
QY	2701	GCTGTCCTAGACGTAATCATNGCTCATAGCTGTTTCTCTGTGTGAATATGTTATPCGCTCACA	2760	
Db	78	GCAAGCTTGGCGTAAATCATNGTCTCATAGCTGTTTCTCTGTGTGAATATGTTATPCGCTCACA	137	
QY	2761	ATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCTCGSGGTGCTATATGAGTG	2820	
Db	138	ATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCTCGSGGTGCTATATGAGTG	197	
QY	2821	AGCTAACTCACATTAATTTGGCTTCGCTCACTGCGCCGTTTCCAGTCGGGAACCTCTCG	2880	
Db	198	AGCTAACTCACATTAATTTGGCTTCGCTCACTGCGCCGTTTCCAGTCGGGAACCTCTCG	257	
QY	2881	TGCCAGCTTGCATTAATAAATCGGCCAACGCGCGGGAGAGCGGTTTTCGTTATTTGGCGCG	2940	
Db	258	TGCCAGCTTGCATTAATAAATCGGCCAACGCGCGGGAGAGCGGTTTTCGTTATTTGGCGCG	317	
QY	2941	TCCTCCGCTTCTCGCTCACTGA	3000	
Db	318	TCCTCCGCTTCTCGCTCACTGA	377	
QY	3001	TCAGCTCAC-TCAAAGCGGTAAATACGGTTATCCACAGATCAGGGGATTAACGACGAGAAA	3059	
Db	378	TCAGCTCACTTTATAGCGCGTAAATACGGTTATCCACAGATCAGGGGATTAACGACGAGAAA	437	
QY	3060	GAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAAACCGTAAAAAGCCGCGTGTCTGGC	3119	
Db	438	GACATGTGAGCAAAAGCCAGCAAAAGCCAGGAAACCGTAAAAAGCCGCGTGTCTGGC	497	
QY	3120	GTTTTTCATAGGCTCGCCCGCTGACGAGCATCACAAAAATCGACGCTCAAAGTCAGAG	3179	
Db	498	GTTTTTCATAGGCTCGCCCGCTGACGAGCATCACAAAAATCGACGCTCAAAGTCAGAG	557	
QY	3180	GTGCGGAAACCCGACAGGACTATAAGATACGAGCGGTTTCCCGCTGGAGAGTCCCTCGT	3239	
Db	558	GTGCGGAAACCCGACAGGACTATAAGATACGAGCGGTTTCCCGCTGGAGAGTCCCTCGT	617	
QY	3240	CGCGTCTCCTGTTCCGACCCCTGCGGCTTACGGATACCTGTCGCGCTTCTCCCTTCGGG	3299	
Db	618	CGCGTCTCCTGTTCCGACCCCTGCGGCTTACGGATACCTGTCGCGCTTCTCCCTTCGGG	677	
QY	3300	AAGCGTGGCGCTTCTCATAGCTCACGCTGTAGTATCTCAGTTCGGTGTAGTGTCTCG	3359	
Db	678	AAGCGTGGCGCTTCTCATAGCTCACGCTGTAGTATCTCAGTTCGGTGTAGTGTCTCG	737	
QY	3360	CTCCAAAGCTGGGCTGTGCAGAAACCCCGCTTACGCCGACCGCTGGCGCTTATCCGG	3419	
Db	738	CTCCAAAGCTGGGCTGTGTGCAGAAACCCCGCTTACGCCGACCGCTGGCGCTTATCCGG	797	
QY	3420	TAACTATCGTCTTGAAGTCCAAACCGGTAAAGACGACTTATCGCCACTGGCAGCAGCCAC	3479	
Db	798	TAACTATCGTCTTGAAGTCCAAACCGGTAAAGACGACTTATCGCCACTGGCAGCAGCCAC	857	
QY	3480	TGCTAACAGGATTAAGACAGCGAGGTATGTAGCGGCTGCTACAGATTCCTTGAAGTGGTG	3539	
Db	858	TGCTAACAGGATTAAGACAGCGAGGTATGTAGCGGCTGCTACAGATTCCTTGAAGTGGTG	917	
QY	3540	GCCTAACTACGGCTACACTAGAAAGACAGTATTTGGTATCTGCGGCTCTGCTGAAGCCAGT	3599	
Db	918	GCCTAACTACGGCTACACTAGAAAGACAGTATTTGGTATCTGCGGCTCTGCTGAAGCCAGT	977	
QY	3600	TACCTTCGG--AAAAGAGTTGTAGCTCTTGATCCGGCAAAACAAACC	3645	
Db	978	TACCTTCGG--AAAAGAGTTGTAGCTCTTGATCCGGCAAAACAAACC	1025	

RESULT 10
CG392995
LOCUS

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DEFINITION ZMMBBc0004E12f ZMMBBc (EcoRI) Zea mays subsp. mays genomic clone
ZMMBBc0004E12 5', genomic survey sequence.
ACCESSION CG392995
VERSION CG392995.1
KEYWORDS GSS.
SOURCE CG392995.1 GI:34336220
ORGANISM Zea mays subsp. mays (maize)
Ze mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 996)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Rouzard,K., Fuku,G., Yu,Y., Wang,R. and Messing,J.
Sequencing of the maize genome at PGIR (2003b)
Unpublished (2003)
Contact: Bharti.A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 11.
Location/Qualifiers
1..996
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/mol_type="genomic DNA"
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/clone="ZMMBBc0004E12"
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/note="vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRT"
FEATURES
source

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ORIGIN	Query Match	17.0%;	Score 898.8;	DB 29;	Length 996;
	Best Local Similarity	98.7%;	Pred. No. 1.9e-208;		
	Matches 906;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;
QY	2701	GCCTGCTPAGACGTAATCATGGCTCATAGCTGTTTCCTGTGTGAAATGTTATCCGGCTCACA	2760		
Db	79	GCAAGCTTGCGTAATCATGGCTATAGCTGTTTCCTGTGTGAAATGTTATCCGGCTCACA	138		
QY	2761	ATTCCACACAAACATACGAGCGGGAAGCATAAAGTGTAAGCCTGGGGTGCCCTAATCATGCT	2820		
Db	139	ATTCCACACAAACATACGAGCGGGAAGCATAAAGTGTAAGCCTGGGGTGCCCTAATCATGCT	198		
QY	2821	AGCTAACTCACATTAATTGGGTTGCGCTCACTGCCCGCTTTCACGTCCGGAAACCTGTGCG	2880		
Db	199	AGCTAACTCACATTAATTGGGTTGCGCTCACTGCCCGCTTTCACGTCCGGAAACCTGTGCG	258		
QY	2881	TGCAGCTGCATTAAATGAATTCGGCCAAACGCGCGGGAGAGCGGTTTTCGPTATTGGCGCG	2940		
Db	259	TGCAGCTGCATTAAATGAATTCGGCCAAACGCGCGGGAGAGCGGTTTTCGPTATTGGCGCG	318		
QY	2941	TCCTTCGGCTTCCTCGCTCACTGACTCGCTCGGCTCGGTCGGTTCGGCTCGCGGAGCGGTA	3000		
Db	319	TCCTTCGGCTTCCTCGCTCACTGACTCGCTCGGCTCGGTCGGTTCGGCTCGCGGAGCGGTA	378		
QY	3001	TCAGCTCACTCAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCAGGAAG	3060		
Db	379	TCAGCTCACTCAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCAGGAAG	438		
QY	3061	AACATGTGACAAAAGGCCAGCAAAAGGCCAGAAACCGTAAAAAGGCGGTTCCTGCGCG	3120		
Db	439	AACATGTGACAAAAGGCCAGCAAAAGGCCAGAAACCGTAAAAAGGCGGTTCCTGCGCG	498		
QY	3121	TTTTTCCATAGGCTCGCGCCCTCGACGAGCATCAAAAAATACGACCTCAAGTCAGAGG	3180		

499 TTTTCCATAGGCTCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGG 558
 3181 TGCGGAAACCCGACAGGACTATAAGATACCAAGCGTTTCCCTCGGAAAGCTCCCTCGTG 3240
 559 TGCGGAAACCCGACAGGACTATAAGATACCAAGCGTTTCCCTCGGAAAGCTCCCTCGTG 618
 3241 CGCTCTCTGTTCCGACCCCTCGGCTTACGGATACCTGTCGCGCTTCTCCCTCGGGA 3300
 619 CGCTCTCTGTTCCGACCCCTCGGCTTACGGATACCTGTCGCGCTTCTCCCTCGGGA 678
 3301 AGCGTCGCGCTTCTCATAGCTCACGCTGAGTATCTCAGTTCGGTGTAGGTCGTTCCG 3360
 679 AGCGTCGCGCTTCTCATAGCTCACGCTGAGTATCTCAGTTCGGTGTAGGTCGTTCCG 738
 3361 TCCAAAGCTGGTGTGTGACGAAACCCCGGTTTACGCGGACCGCTGCGCTTATCCGGT 3420
 739 TCCAAAGCTGGTGTGTGACGAAACCCCGGTTTACGCGGACCGCTGCGCTTATCCGGT 798
 3421 AACTATCGTCTGAGTCCAAACCGGTAAGACACGACTTATCGCACTGGCGAGCACT 3480
 799 AACTATCGTCTGAGTCCAAACCGGTAAGACACGACTTATCGCACTGGCGAGCACT 858
 3481 GGTAAACAGATTACGAGGAGGAGTATGTAGGCGGTGCTACAGAGTCTTTGAAAGTGTGG 3540
 859 GGTAAACAGATTACGAGGAGGAGTATGTAGGCGGTGCTACAGAGTCTTTGAAAGTGTGG 918
 3541 CCTAATACCGGTACACTAGAAAGACAGTATTTGGTATCTGCGCTTCTGTAAGCCAGTT 3600
 919 CCTAATACCGGTACACTAGAAAGACAGTATTTGGTATCTGCGCTTCTGTAAGCCAGTT 978
 3601 ACCTTCGGAAGAAAGAGTT 3618
 979 TACCTCCGGAAGAGGT 996

RESULT 11
 CK291799/c
 LOCUS
 DEFINITION
 EST754513 Nicotiana benthamiana mixed tissue cDNA library,
 normalized, full-length Nicotiana benthamiana cDNA clone NBMC477 5',
 end, mRNA sequence.
 CK291799
 CK291799.1 GI:39872608
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Nicotiana benthamiana
 Nicotiana benthamiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Nicotiana.
 1 (bases 1 to 933)
 Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
 Staskiewicz,B., Jin,H. and Baker,B.
 Generation of EST sequences from Nicotiana benthamiana
 Unpublished (2003)
 Other ESTs: EST754514
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: ATT TAG GTG ACA CTA TAG.
 Location/Qualifiers
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 /organism="Nicotiana benthamiana"
 /mol_type="mRNA"
 /db_xref="taxon:4100"
 /clone="NBMC477"
 /tissue_type="abiotic and biotic stress-treated leaves,
 callus tissue and root tissue"
 /lab_host="DH10B-TonA"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA
 library, normalized, full-length"
 /note="vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;

supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match 16.8%; Score 886.4; DB 14; Length 933;
 Best Local Similarity 99.9%; Pred. No. 2e-205;
 Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4044 GCCCAACCTTTCATAGAGGCGCGGTGGAATCGAAATCTCGTGATGGCAGGTGGCGGT 4103
 Db 933 GCCCAACCTTTCATAGAGGCGCGGTGGAATCGAAATCTCGTGATGGCAGGTGGCGGT 874
 QY 4104 CGCTTGGTCCGTCATTTCCGAACCCCGAGTCCCGCTCAGAAGAACTCGTCAAGAAAGCGGA 4163
 Db 873 CGCTTGGTCCGTCATTTCCGAACCCCGAGTCCCGCTCAGAAGAACTCGTCAAGAAAGCGGA 814
 QY 4164 TAGAAGCGGATGCGCTGCGAATCGGAGCGCGGATACCGTAAAGACAGAGAGCGGTCA 4223
 Db 813 TAGAAGCGGATGCGCTGCGAATCGGAGCGCGGATACCGTAAAGACAGAGAGCGGTCA 754
 QY 4224 GCCCATTCGCGGCAAGCTCTTCAGCAATATCAGGGTAGCCAAAGCTATGCTCTGATAG 4283
 Db 753 GCCCATTCGCGGCAAGCTCTTCAGCAATATCAGGGTAGCCAAAGCTATGCTCTGATAG 694
 QY 4284 CGGTCCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACC 4343
 Db 693 CGGTCCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTTCCACC 634
 QY 4344 ATGATATTCGCGCAAGCAGGATCGCCATGGGTCAACGACGAGATCTCTCGCGTCGGGATG 4403
 Db 633 ATGATATTCGCGCAAGCAGGATCGCCATGGGTCAACGACGAGATCTCTCGCGTCGGGATG 574
 QY 4404 CGGCGCTTGTAGCCTTGGCGAAACAGTTCGGCTGGGCGGAGCCCTGATGCTCTCTGTCGAGA 4463
 Db 573 CGGCGCTTGTAGCCTTGGCGAAACAGTTCGGCTGGGCGGAGCCCTGATGCTCTCTGTCGAGA 514
 QY 4464 TCATCTGTATCGACAAGACCGGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTC 4523
 Db 513 TCATCTGTATCGACAAGACCGGCTTCCATCCGAGTACGTCTCGCTCGATGCGATGTTTC 454
 QY 4524 GCTTGGTGGTTCGAATGGGCGAGTAGCCGATCAAGCGTATGACGCCCGCGCATTTGCATCA 4583
 Db 453 GCTTGGTGGTTCGAATGGGCGAGTAGCCGATCAAGCGTATGACGCCCGCGCATTTGCATCA 394
 QY 4584 GCCATGATGATATCTTCTCGGAGGACAGGTGAGATGACAGAGATCTCTGCCCCGCGC 4643
 Db 393 GCCATGATGATATCTTCTCGGAGGACAGGTGAGATGACAGAGATCTCTGCCCCGCGC 334
 QY 4644 ACTTCGCGCCATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAAGCTCGAGCAGAGTCCG 4703
 Db 333 ACTTCGCGCCATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAAAGCTCGAGCAGAGTCCG 274
 QY 4704 CAAGAAAGCGCCGCTGTCGGCGAGCCAGATAGCCGCGTCTGCTCTGAGTTCATTC 4763
 Db 273 CAAGAAAGCGCCGCTGTCGGCGAGCCAGATAGCCGCGTCTGCTCTGAGTTCATTC 214
 QY 4764 AGGGCAGCGGACAGGTGGTCTTCACAAAAGAACCGGGCGCCCTGCGCTGACAGCCGG 4823
 Db 213 AGGGCAGCGGACAGGTGGTCTTCACAAAAGAACCGGGCGCCCTGCGCTGACAGCCGG 154
 QY 4824 AACACGGCGGATCAGAGCAGCCGATTTGTCTGTTGTGCCAGTATAGCCGAAATAGCCTC 4883
 Db 153 AACACGGCGGATCAGAGCAGCCGATTTGTCTGTTGTGCCAGTATAGCCGAAATAGCCTC 94
 QY 4884 TCCACCCCAAGCGCGGAGAACCTCGCTGCGAATCCATCTTTGTTCAATC 4931

Db	93	TCCACCCAGCGCGGAGAACCTCGTGCAATCATCTGTCAATC	46
RESULT 12			
CG392916			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
QY	2701	GCTGTCTAGACGTAATCATCGTTCATAGCTGTTTCCTGTGTGTAATGTTATCGCTCACA	2760
Db	67	GCAGCTTGGCGTAATCATGCTTCAGTCTGTTTCCTGTGTGTAATGTTATCGCTCACA	126
QY	2761	ATTCCACACAATACGACGCGGAAGCATAAAGTGTAAAGCTGGGTCCTAAAGCAGTG	2820
Db	127	ATTCCACACAATACGACGCGGAAGCATAAAGTGTAAAGCTGGGTCCTAAAGCAGTG	186
QY	2821	AGCTAACTACATTAATGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAACCTGTGC	2880
Db	187	AGCTAACTACATTAATGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAACCTGTGC	246
QY	2881	TGCGACGTCATTAATGAATCGGCCAACCGGGGAGAGCGGTTTGGGTATGCGGC	2940
Db	247	TGCCAGCTCAITTAATGAATCGGCCAACCGGGGAGAGCGGTTTGGGTATGCGGC	306
QY	2941	TCTTCGCTTCCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	3000
Db	307	TCTTCGCTTCCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	366
QY	3001	TAGCTCACTCAAGCGCGTAATACGGTTATCCACAGATACAGGGGATAACGAGGAAG	3060
Db	367	TCAGCTCACTCAAGCGCGTAATATGTTATCCACAGATACAGGGGATAACGAGGAAG	426


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/mol_type="mRNA"
/cultivar="Westar"
/db_xref="taxon:3708"
/clone="Bn01b 02008"
/tissue_type="fourth leaf"
/dev_stage="3 weeks seedling grown at room temperature"
/clone_lib="Bn01b AAFB EORC transgenic Brassica napus_ove
expressing BNCBF17 constitutively frost_tolerant"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
Site 2: XhoI; Germinated in soil flats and seedlings grown
for 3 weeks in a Conviron E-15 cabinet set at 20°C/16 hr
light (250 Em-2sec-1) and 16 °C/ 8 hr dark. Fourth leaves
collected at 9 am and immediately frozen."

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ORIGIN

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Query Match 16.6%; Score 875; DB 14; Length 925;
Best Local Similarity 98.6%; Pred. No. 1.2e-202;
Matches 886; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 2701 GCTGCTAGACGTAATCATGTCATAGCTGTTTCCGTGTGTAATTTGTTATCCGCTCACA 2760
DB 898 GCGCGCTTGGCGTAATCATGTCATAGCTGTTT-CTGTGTGAAATTTGTTATCCGCTCACA 840
QY 2761 ATTCCACACACATACGAGCGGAGCATAAAGTGTAAAGCCTGGGTGCTTAATGAGTG 2820
DB 839 ATTCCACACACATACGAGCGGAGCATAAAGTGTAAAGCCTGGGTGCTTAATGAGTG 780
QY 2821 AGCTAACTACATTAATTGCGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGTGTCG 2880
DB 779 AGCTAACTACATTAATTGCGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGTGTCG 720
QY 2881 TGGCAGCTGATTAATGAATCGGCAACGCGCGGGAGAGCGGTTTGGCTATTGGCGGC 2940
DB 719 TGGCAGCTGATTAATGAATCGGCAACGCGCGGGAGAGCGGTTTGGCTATTGGCGGC 660
QY 2941 TCTTCCGCTTCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
DB 659 TCTTCCGCTTCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 3001 TCAGCTCACTCAAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGAGGAAG 3060
DB 599 TCAGCTCACTCAAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGAGGAAG 540
QY 3061 AACATGTGACAAAGCGCAGCAAAAGCGCGAGAACCGTAAAGAGCGCGGTTCTGCGGC 3120
DB 539 AACATGTGACAAAGCGCAGCAAAAGCGCGAGAACCGTAAAGAGCGCGGTTCTGCGGC 480
QY 3121 TTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCAGCGCTCAAGTCAGAGG 3180
DB 479 TTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCAGCGCTCAAGTCAGAGG 420
QY 3181 TGGCGAAACCCGACGAGGACTATAAGATACCAGCGGTTTCCCTGGAAGTCCTCTCGTG 3240
DB 419 TGGCGAAACCCGACGAGGACTATAAGATACCAGCGGTTTCCCTGGAAGTCCTCTCGTG 360
QY 3241 CGCTCTCTGTTCGACCGCTGCTACCGGATACCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
DB 359 CGCTCTCTGTTCGACCGCTGCTACCGGATACCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 3301 AGCGTGGCGCTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGC 3360
DB 299 AGCGTGGCGCTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGC 240
QY 3361 TCCAAGCTGGGCTGTGTGACAGAACCCCGCTTACGCCGACCGCTGCGGCTTATCCCGT 3420
DB 239 TCCAAGCTGGGCTGTGTGACAGAACCCCGCTTACGCCGACCGCTGCGGCTTATCCCGT 180
QY 3421 AACTATGCTTGTAGTCAACCCGCTAAGACAGCACTTATCGCACTGCGAGCGCACT 3480
DB 179 AACTATGCTTGTAGTCAACCCGCTAAGACAGCACTTATCGCACTGCGAGCGCACT 120
QY 3481 GGTAAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGG 3540

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DB 119 GCTAAACARGATTASCAGACGCGAGGTATGTAGCGGTGTACAGAGTTCTTSAAGTGGTGG 60
QY 3541 CTTAACTACGCTACACTAGAGAACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGT 3599
DB 59 CTTAACTACGCTACACTAGAGAACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGT 1

RESULT 14
CF269652 1073 bp mRNA linear EST 13-AUG-2003
LOCUS Fcylcold844 Fragilariopsis cylindrus SMART cDNA library (Clontech)
DEFINITION Fragilariopsis cylindrus cDNA clone Antarctic 5', mRNA sequence.
ACCESSION CF269652
VERSION CF269652.1 GI:33631539
KEYWORDS EST
SOURCE Fragilariopsis cylindrus
ORGANISM Fragilariopsis cylindrus
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis.
1 (bases 1 to 1073)
Mock, T. and Valentin, K.
EST analysis of freezing tolerance in the Antarctic diatom
Fragilariopsis cylindrus: Detection of numerous cold adaptation
related genes and gene transfer events
Unpublished (2003)
Contact: Mock T
Biological Oceanography
Alfred-Wegener-Institute for Polar and Marine Research
Am Handelshafen 12, D-27570 Bremerhaven, Germany
Tel.: +49 471 4831 1893
Fax: +49 471 4831 1425
Email: tmock@awi-bremerhaven.de
sequence with unknown function
PCR Primers
FORWARD: 5'lambdaTriplex2
BACKWARD: 3'lambdaTriplex2
Seq primer: ctcgggaagcgccattgtgtggt.
FEATURES
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(Clontech)"
/note="Vector: pTriplex2; total polyA was used for
first-strand synthesis with SMART IV oligos and CDS
III/3 PCR primer. Double strand cDNA synthesis was done by
LD PCR using the following program: 95oC for 5 min
denaturation and subsequent 20 cycles at 95oC (2min) and
68oC (6min). After SfiI digestion the cDNA was
fractionated with CHROMA Spin-400 columns. These cDNAs
were ligated overnight into pTriplex2 vectors."

ORIGIN
Query Match 16.4%; Score 866.2; DB 14; Length 1073;
Best Local Similarity 96.4%; Pred. No. 1.9e-200;
Matches 927; Conservative 0; Mismatches 28; Indels 7; Gaps 4;

QY 2839 GCGTTGCGCTCACTGCCGCTTTCAGTCGGGAAACCTGTGTCGCCAGCTCATTAATGA 2898
DB 1 GCTTCTTGCTCACTGCCGCTTTCAGTCGGGAAACCTGTGTCGCCAGCTCATTAATGA 60
QY 2899 ATCGGCCAACCGCGGGGAGAGCGGTTTGGGTATTTGGCGCTTTCGCTTCTTCGCTC 2958
DB 61 ATCGGCCAACCGCGGGGAGAGCGGTTTGGGTATTTGGCGCTTTCGCTTCTTCGCTC 120
QY 2959 ACTGACTCGCTCGCTCGCTCGTTCGGCTGCGGCGAGCGGTATCAGTCACTCAAGAGCG 3018
DB 121 ACTGACTCGCTCGCTCGCTCGTTCGGCTGCGGCGAGCGGTATCAGTCACTCAAGAGCG 180
QY 3019 GTAATACGGTTATCCACAGATCAGGGGATACGAGGAGAAACATGTGAGCAAAAGGC 3078

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Db 181 GTAAACGGTTATTCACAGAAATCAGGGGATACGAGGAAAGAAATGTGACAAAAGGC 240
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Db 241 CAGCAAAAGGCGCAGGAACCGTAAAAAGGCGGTTGCTGGCGTTTTTTCATAGGCTCCGC 300
QY 3139 CCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA 3198
Db 301 CCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA 360
QY 3199 CTATAAGATACCGGCGTTTCCCGCTCGAAGCTCCCTCGCGGTCTCTCTTCCGACC 3258
Db 361 CTATAAGATACCGGCGTTTCCCGCTCGAAGCTCCCTCGCGGTCTCTCTTCCGACC 420
QY 3259 CTGCGGCTTACCGGATACCTGTCCGCTTTCCTCCCTCGGGAAGCGTGGCGTTTCTCAT 3318
Db 421 CTGCGGCTTACCGGATACCTGTCCGCTTTCCTCCCTCGGGAAGCGTGGCGTTTCTCAT 480
QY 3319 AGCTCACGCTGTAGTATCTCAGTTTCGGGTGAGTTCGCTCCAAAGCTGGGCTGTGTG 3378
Db 481 AGCTCACGCTGTAGTATCTCAGTTTCGGGTGAGTTCGCTCCAAAGCTGGGCTGTGTG 540
QY 3379 CACGAACCCCGGTTACCGCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCC 3438
Db 541 CACGAACCCCGGTTACCGCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCC 600
QY 3439 AACCCGGTAAACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGA 3498
Db 601 AACCCGGTAAACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGA 660
QY 3499 GCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTTAACTACNGGCTACA 3556
Db 661 GCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTTAACTACNGGCTACA 720
QY 3557 CTAGAAGAACA-GTATTTGGTATCT-GCGCTCTGCTGAGCC--AGTACTCTTCGNA 3611
Db 721 CTAGAAGAACAAGTATTTGGTATCTGCGCTCTGCTGAGCCAGTAACTACNGGCTACA 780
QY 3612 AAGAGTTGGTACGCTTTCGATCCGCGCAAAACACACCGCTGGTAGCGGTGTTTTTGT 3671
Db 781 AAGAGTTGGTACGCTTTCGATCCGCGCAAAACACACCGCTGGTAGCGGTGTTTTTGT 840
QY 3672 TTGAAGCAGCAGATTAACGCGCAGAAAAGGATCTCAAGAGATCTTTGATCTTTTC 3731
Db 841 TTGAAGCAGCAGATTAACGCGCAGAAAAGGATCTCAAGAGATCTTTGATCTTTTC 900
QY 3732 TACGGGCTGACGCTCAGTGGACGAACTCAGTTAAGGATTTGGTCAATGAGATT 3791
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QY 3792 AT 3793
Db 961 AT 962
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RESULT 15
CG835880 1056 bp DNA linear GSS 12-NOV-2003
LOCUS ZMMBc0212F14f ZMMBc (EcoRI) Zea mays subsp. mays genomic clone
DEFINITION ZMMBc0212F14 5', genomic survey sequence.
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ACCESSION CG835880
VERSION CG835880.1 GI:38300279
KEYWORDS GSS.
SOURCE Zea mays subsp. mays (maize)
ORGANISM Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1056)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PGIR (2003c)
```

JOURNAL
COMMENT

Unpublished (2003)
Contact: Bharti, A. K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: 17

Class: BAC ends
High quality sequence start: 74.

FEATURES
source

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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Query Match 16.1%; Score 849; DB 29; Length 1056;
Best Local Similarity 95.8%; Pred. No. 3.1e-196;
Matches 936; Conservative 0; Mismatches 35; Indels 6; Gaps 6;
QY 2701 GCTGCTAGACGTAATCATGTCTATAG-CTGTTTCTCTGTGAAATTTTATCCGCTCAC 2759
Db 80 GCAAGCTTGGCGTAATCATGCAATAGAGGTTTCTCTGTGAAATTTTATCCGCTCAC 139
QY 2760 AATTCCACACACATACAGCCGAGCATTAAGTGAAGCTGGGTGCTTAATAGT 2819
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QY 2820 GAGCTAATCATTAATTTGGTTGCGTCTACTCCCGCTTTCCAGTCGGGAAACCTGTC 2879
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QY 2880 GTGCCAGCTGANTPAATGAATCGGCCAACCGCGGGAGAGCGGTTTTCGCTATTGGGCG 2939
Db 260 GTGCCAGCTGANTPAATGAATCGGCCAACCGCGGGAGAGCGGTTTTCGCTATTGGGCG 319
QY 2940 CTCTTCGCTTCTCCGCTCACTGACTGCTGCGTCTCGGTCGCTCGGTCGGGCGAGCGGT 2999
Db 320 TTCTTCGCTTCTCCGCTCACTGACTGCTGCGTCTCGGTCGCTCGGTCGGGCGAGCGGT 379
QY 3000 ATCAGCTCACTCAAAAGCGGTAAATACGTTATCCACAGAAATCAGGGATACGCGAGGAA 3059
Db 380 ATCAGCTCACTTTTGTCTGTATACGTTATCCACAGAAATCAGGGATACGCGAGGAA 439
QY 3060 GAACATGTAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAA 3119
Db 440 GAACATGTAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAAAGGCCAGCAAA 499
QY 3120 GTTTTTCATAGGCTCGCCCGCTCTGACGAGCATCAAAAATTCAGCTCAAGTCAGAG 3179
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QY 3300 AAGGTGGCGCTTCTCATAGCTACGCTGTAGTATCTCAGTTTCGGGTAGGTCGTTG 3359
Db 680 AAGGTGGCGCTTCTCATAGCTCAGCTGTAGTATCTCAGTTTCGGGTAGGTCGTTG 739

QY 3360 CTCGAGCTGGGCTGTGTCACGACCCCGCTTCAGCCGACCGCTGCGCTTATCCGG 3419
Db |||||
740 CTCGAAGCTGGGCTGTGTCACGACCCCGCTGTTCAGCCCGACCGCTGCGCTTATCCGG 799
QY 3420 TAACTATCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCCAC 3479
Db |||||
800 TAACTATCGTCTTGAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGGCAGCAG-CAC 858
QY 3480 TGGTAACAGGATTAGCAGAGCGAGGTATGTAGG-CGGTGCTACAGAGTCTTTGAAGTGGT 3538
Db |||||
859 TGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTTGAAGTGGT 918
QY 3539 GGCCTAACTACGCTACACTAGNAGACAGTATTT-GGTATCTGCGCTCTGCTGAAGCCA 3597
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919 -GTCTAACTACGCTACACTAGNAGACAGTATTTGGGTATCTGCGCTCTGCTGAAGCCA 977
QY 3598 GTTACCTTCGGAAAAAGAGTT-GGTAGCTCTTGATCCGGCAAAACCAACCGCTGCTAG 3656
Db |||||
978 GTTACTTTGGAAAAAGAGTTGGGTAGCTCTTGATCCGGCAAAACCAACCGCTGCTAG 1037
QY 3657 CGGTGGTTTTTTTGGTTT 3673
Db |||||
1038 GCGGTGGTTTTTTTGT 1054

Search completed: August 4, 2004, 14:24:48
Job time : 12197 secs